

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
 C58." ;  
 RL Science 294:2317-2323(2001).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX MEDLINE=2608551; PubMed=11743194; DOI=10.1126/science.1066803;  
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
 RA Qurollo B., Goldman B.S., Cao Y., Askewazi M., Hailing C., Mullin L.,  
 RA Houmlet K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,  
 RA Wolam C., Allinger M., Doughy D., Scott C., Lappas C., Markelz B.,  
 RA Flanagan C., Crowell C., Garson J., Lomo C., Sear C., Strub G.,  
 RA Cielo C., Slater S.,  
 RT "Genome sequence of the plant pathogen and biotechnology agent  
 Agrobacterium tumefaciens C58." ;  
 RL Science 294:2323-2328(2001).  
 CC -1- SIMILARITY: Belongs to the ABC transporter family.  
 DR EMBL, AE009247; AA14396.1; -; Genomic DNA.  
 DR EMBL, AE008366; AA39206.1; -; Genomic DNA.  
 DR PIR, AF2947; AF2947.  
 DR PIR, D98335; D98335.  
 DR GO, GO:0016020; C:membrane; IEA.  
 DR GO, GO:0005524; F:ATP binding; IEA.  
 DR GO, GO:0016887; F:ATPase activity; IEA.  
 DR GO, GO:0016787; F:hydrolase activity; IEA.  
 DR GO, GO:0000166; F:nucleotide binding; IEA.  
 DR GO, GO:0006810; P:transport; IEA.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003439; ABC\_transp\_like.  
 DR Pfam: PF00005; ABC\_tran.1.  
 DR ProDom: PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER\_1; UNKNOWN\_1.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Complete proteome; Nucleotide-binding; Transport.  
 SQ SEQUENCE 277 AA; 29733 MW; 282D3A83B0D9124 CRC64;  
 QY Query Match 49.5%; Score 51; DB 2; Length 277;  
 Best Local Similarity 58.8%; Pred. No. 26;  
 Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
 DB 5 DNAAVLEGSIVKVTGANG 21  
 25 DGAIRAGSLTAVVGANG 41  
 RESULT 5  
 Q8KFB5 CHLITE PRT; 361 AA.  
 ID Q8KFB5; CHLITE PRELIMINARY;  
 AC Q8KFB5;  
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Iron(III) ABC transporter, ATP-binding protein, putative.  
 GN OrderedOcunNames=CT0412;  
 OS Chlorobium tepidum.  
 OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;  
 CC Chlorobaculum.  
 OK NCBI\_TaxId=1097;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=TLS / ATCC 49652 / DSM 12025;  
 RX MEDLINE=22103685; PubMed=12093901; DOI=10.1073/pnas.132181499;  
 RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,  
 RA Dodson R.J., Deboy R.T., Gwinn M.L., Nelson W.C., Haft D.H.,  
 RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.F., Yang F.,  
 RA Holt I.E., Umayam L.A., Mason T.M., Brenner M., Shea T.P.,  
 RA Parksey D.S., Nierman W.C., Feldblum T.V., Hansen C.L., Craven M.B.,  
 RA Redunc K.A., Venter J.C., Tettelin H., Bryant D.A., Fraser T.M.,  
 RA "The complete genome sequence of Chlorobium tepidum TLS, a  
 photoautotrophic, anaerobic, green-sulfur bacterium." ;  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).  
 RL -1- SIMILARITY: Belongs to the ABC transporter family.

DR EMBL; AB006470; AAM71658.1; -; Genomic DNA.  
 DR TIGR; CT0412; -;  
 DR GO, GO:0016020; C:membrane; IEA.  
 DR GO, GO:0005524; F:ATP binding; IEA.  
 DR GO, GO:0016887; F:ATPase activity; IEA.  
 DR GO, GO:0016787; F:hydrolase activity; IEA.  
 DR GO, GO:0000166; F:nucleotide binding; IEA.  
 DR GO, GO:0006810; P:transport; IEA.  
 DR InterPro: IPR003593; AAA\_ATPase.  
 DR InterPro: IPR003439; ABC\_transp\_like.  
 DR Pfam: PF00005; ABC\_tran.1.  
 DR ProDom: PD000006; ABC\_transporter; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00893; ABC\_TRANSPORTER\_2; 1.  
 KW ATP-binding; Complete proteome; Membrane; Nucleotide-binding;  
 Transport.  
 SQ SEQUENCE 361 AA; 39746 MW; 784BFB619DB69D3D CRC64;  
 QY Query Match 49.5%; Score 51; DB 2; Length 361;  
 Best Local Similarity 55.0%; Pred. No. 33;  
 Matches 11; Conservative 2; Mismatches 7; Indels 0; Gaps 0;  
 DB 2 AIPDNAAVLEGSIVKVTGANG 21  
 244 AIPESLVLEGHLEKAFSRNG 263  
 RESULT 6  
 ID 06SDJ1 BACLD PRT; 396 AA.  
 AC 06SDJ1\_062P10;  
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)  
 DE ywbd (SAM (and some other nucleotide) binding motif, PUA domain).  
 GN Name=ywbd; OrderedOcunNames=BI03857, BI04060;  
 OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OK NCBI\_TaxId=279010;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15383718; DOI=10.1159/000079829;  
 RA Veith B., Herzberg C., Steckel S., Reschke J., Maurer K.H.,  
 RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Mehl R.,  
 RA Ehrenreich A., Gottschalk G.;  
 RT "The complete genome sequence of Bacillus licheniformis DSM13, an  
 organism with great industrial potential." ;  
 RT J. Mol. Microbiol. Biotechnol. 7:204-211(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RX PubMed=15461803; DOI=10.1186/gb-2004-5-10-r77;  
 RA Rey M.W., Ramalhya P., Nelson B.A., Brody-Karpin S.D., Zaretzky E.J.,  
 RA Tang M., Lopez de Leon A., Xiang H., Gueti V., Clausen I.G.,  
 RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,  
 RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galleron N.,  
 RA Ehrlich S.D., Berka R.M.;  
 RT "Complete genome sequence of the industrial bacterium Bacillus  
 licheniformis and comparisons with closely related Bacillus species." ;  
 RT Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).  
 DR EMBL, AE017333; AAU42873.1; -; Genomic DNA.  
 DR EMBL, CP000002; AAU25501.1; -; Genomic DNA.  
 DR GO, GO:0003723; F:rRNA binding; IEA.  
 DR GO, GO:0008757; F:s-denosylmethionine-dependent methyltransf. .; IEA.  
 DR InterPro: IPR002478; PUA.  
 DR InterPro: IPR000051; SAM\_bd.  
 DR SMART; SM00359; PUA; 1.  
 DR PROSITE; PS50890; PUA; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 396 AA; 44897 MW; C1FFDIAJCSSEFFZ2AE CRC64;  
 QY Query Match 49.5%; Score 51; DB 2; Length 396;  
 Best Local Similarity 47.1%; Pred. No. 37;  
 Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

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Oy      5 DNAAVLEGSVLYVTGANG 21
       : : : : : : : : : :
Db      30 ENGIXEGSLIRITBENG 46

RESULT 7
O45000 CAEBL
ID O45000 CAEBL PRELIMINARY; PRT; 1620 AA.
AC O45000
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interest in neurexin-like protein 1.
GN Name=itx-1; ORFName=W03D8.6;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peleoderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Brice1 N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; AF043702; AAK21492.3; -, Genomic_DNA.
DR Ensembl; W03D8.6; Caenorhabditis elegans.
DR WormBase; WBGene00002174; itx-1.
DR WormPep; W03D8.6; CE32737.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR012680; Laminin_G_2.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00181; EGF_2.
DR SMART; SM00282; Lamin_3.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 3.
DR PROSITE; PS50025; LAM_G_DOMAIN; 4.
KW Complete proteome.
SQ SEQUENCE 1620 AA; 180492 MW; 6767E4679CBA04D1 CRC64;

Query Match 49.5%; Score 51; DB 2; Length 1620;
Best Local Similarity 78.6%; Pred. No. 1.5e+02;
Matches 11; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy      1 MAIPDNVLEGSV 14
       : : : : : : : : : :
Db      779 MTIGDNVLEGSV 792

RESULT 8
O4HUZ1 GIBZE
ID O4HUZ1 GIBZE PRELIMINARY; PRT; 368 AA.
AC O4HUZ1
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORName=FG11217.1;
OS Glibberella zae PH-1.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
OX NCBI_TaxID=229533;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PH-1;
RA Bitren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,

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RA Arachchi H.M., Barna N., Baetien V., Bloom T., Boguelavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Canarata J., Chang J.,
RA Choepel Y., Collamore A., Cook A., Cooke P., Corum B., Dearellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,
RA Gardyna S., Gneire S., Graham L., Grand-Pierre N., Hafez N.,
RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
RA Kelle C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
RA Matthews C., Mautceli E., McCarthy M., Melrim J., Menues L.,
RA Michova T., Mienga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
RA Nielsen C.B., Norb C., O'Connor T., O'Donnell P., O'Neill D.,
RA Oliver J., Peterson K., Phunhahng P., Pierre N., Purcell S.,
RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Smitrov S.,
RA Suth C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
RA Talamas J., Teafaye S., Theodore J., Topham K., Travers M.,
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
RA Lander E.;
RT "Fusarium graminearum genome sequence.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1 CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACM01000460; EAA75427.1; -, Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 368 AA; 40538 MW; ADA3963B94946D5 CRC64;

Query Match 49.0%; Score 50.5; DB 2; Length 368;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 14; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

Oy      1 MAIPDNVLEGSVLYVTGANG 21
       : : : : : : : : : :
Db      1 MAIPDNVAVKGSVLYVTGANG 22

RESULT 9
OQMM39 9SEPER
ID OQMM39 9SEPER PRELIMINARY; PRT; 412 AA.
AC OQMM39
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE F1 ATPase alpha subunit (Fragment).
GN Name=atpA;
OS Gnetum sp.
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Gnecophyta; Gnecopsida; Gnecatales; Gnecatales; Gnecum.
OX NCBI_TaxID=3383;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20226063; PubMed=10760278; DOI=10.1073/pnas.97.8.4092;
RA Bowe L.M., Coat G., dePamphilis C.W.;
RT "Phylogeny of seed plants based on all three genomic compartments:
RT extant gymnosperms are monophyletic and Gnecatales' closest relatives
RT are conifers.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4092-4097(2000).
CC -1 SIMILARITY: Belongs to the ATPase alpha/beta chains family.
DR EMBL; AF209109; AAF64667.1; -, Genomic_DNA.
DR HSSP; P19483; 1H8E.
DR SWR; OQMM39; 1-399.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0045461; C:proton-transporting ATP synthase complex; C. . . IEA.
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0046933; F:hydrogen-transporting ATP synthase activity. . . IEA.
DR GO; GO:0046961; F:hydrogen-transporting ATPase activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016820; F:hydrolase activity, acting on acid anhydrid. . . IEA.

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DR GO:0015986; P:ATP synthase coupled proton transport; IEA.
DR GO:0006811; P:ion transport; IEA.
DR GO:0015992; P:proton transport; IEA.
DR InterPro: IPR005294; ATP synthet1 alph.
DR InterPro: IPR004100; ATPase_a/b_N.
DR InterPro: IPR00194; ATPase_a/bcentre.
DR Pfam: PF00006; ATP-synt_ab_1.
DR Pfam: PF02874; ATP-synt_ab_N; 1.
DR TIGRFAMs: TIGR00962; atpA; 1.
DR PROSITE: PS00152; ATPase ALPHA BETA; 1.
KM ATP synthase; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase;
ion transport; Mitochondrion; Nucleotide-binding; Transport.
FT NON_TER 1
SQ SEQUENCE 412 AA; 43993 MW; 824873B6ED21327B CRC64;

Query Match 48.5%; Score 50; DB 2; Length 412;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 5 DNAAEGSLVKTGA 19
Db 45 DTAIEGSIYKRTS 59

RESULT 10
O977A3_GNEGN PRELIMINARY; PRT; 418 AA.
AC O977A3_GNEGN
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE ATPase alpha subunit (Fragment).
GN Name=atp1.
OS Gnetum gnetum (Bago).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Gnepophyta; Gnetales; Gnetales; Gnetales; Gnetales.
OC NCBI_TaxID=3382;
[1]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=20052162; PubMed=1058679; DOI=10.1038/46536;
RA Qiu Y.L., Lee J., Bernasconi-Quadroni F., Soltis D.E., Soltis P.S.,
Zanis M., Zimmer E.A., Chen Z., Savolainen V., Chase M.W.;
"Type earliest angiosperms: evidence from mitochondrial, plastid and
nuclear genomes.";
RT Nature 402:404-407(1999).
CC -1 SIMILARITY: Belongs to the ATPase alpha/beta chains family.
DR EMBL: AF197617; AAF16949.1; -; Genomic_DNA.
DR HSSP: P19483; 1879.
DR SMR: O977A3; 1-418.
DR GO:0005739; C:mitochondrion; IEA.
DR GO:00045261; C:proton-transporting ATP synthase complex, C..; IEA.
DR GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.
DR GO:0005524; F:ATP binding; IEA.
DR GO:0046933; F:hydrogen-transporting ATP synthase activity, .; IEA.
DR GO:0016787; F:hydrolase activity; IEA.
DR GO:0016820; F:hydrolase activity, acting on acid anhydrid. .; IEA.
DR GO:0015986; P:ATP synthase coupled proton transport; IEA.
DR GO:0006811; P:ion transport; IEA.
DR GO:0015992; P:proton transport; IEA.
DR InterPro: IPR005294; ATP synthet1 alph.
DR InterPro: IPR000793; ATPase_a/b_C.
DR InterPro: IPR004100; ATPase_a/b_N.
DR InterPro: IPR000194; ATPase_a/bcentre.
DR Pfam: PF00006; ATP-synt_ab_1.
DR Pfam: PF00306; ATP-synt_ab_C; 1.
DR Pfam: PF02874; ATP-synt_ab_N; 1.
DR TIGRFAMs: TIGR00962; atpA; 1.
DR PROSITE: PS00152; ATPase ALPHA BETA; 1.
KM ATP synthase; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase;
ion transport; Mitochondrion; Nucleotide-binding; Transport.

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FT NON_TER 1
SQ SEQUENCE 418 AA; 44753 MW; 0FE55A3B5722901 CRC64;

Query Match 48.5%; Score 50; DB 2; Length 418;
Best Local Similarity 60.0%; Pred. No. 55;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 5 DNAAEGSLVKTGA 19
Db 44 DTAIEGSIYKRTS 58

RESULT 11
O691P6_ORYSA PRELIMINARY; PRT; 451 AA.
AC O691P6_ORYSA
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Putative aspartic proteinase nepenthesin 1.
GN Name=OSUNBA0039D04.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
[1]
RN NUCLEOTIDE SEQUENCE.
RP Sasaki T., Matsumoto T., Katayose Y.;
RA "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 7, BAC
clone:OSUNBA0039D04.";
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP006753; BAD32124.1; -; Genomic_DNA.
DR Gramene: O691P6; -.
DR GO:0004194; F:pepsin A activity; IEA.
DR GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001461; Peptidase_A1.
DR InterPro: IPR001969; Pept_Asp_AS.
DR Pfam: PF00026; Asp; 1.
DR PRINTS: PR00792; PEPsin.
DR PROSITE: PS00141; ASP PROTEASE; UNKNOWN 1.
SQ SEQUENCE 451 AA; 46440 MW; E7F24FED78353C5E CRC64;

Query Match 48.5%; Score 50; DB 2; Length 451;
Best Local Similarity 62.5%; Pred. No. 60;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 DNAAEGSLVKTGAN 20
Db 243 DSPILFGSLAVTGN 258

RESULT 12
O6B1S4_DEBHA PRELIMINARY; PRT; 1048 AA.
AC O6B1S4_DEBHA
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Similar to CA1657|IPF16022 Candida albicans IPF16022 unknown
function.
GN Ordered locus names=DEHA0608679g;
OS Debaryomyces hansenii (yeast) (Torulasporea hansenii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OC NCBI_TaxID=4959;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 36239 / CBS 767;
RC PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durren P., Casaregola S.,
Latouche I., de Montigny J., Marck C., Neuvéglise C., Talla E.,

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RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,  
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykassen C.,  
 RA Bostrame A., Boyer J., Catroico L., Confanioli F., de Daruvar A.,  
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Gropi A.,  
 RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,  
 RA Karest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,  
 RA Nicand J.-M., Nkoltsi M., Otae S., Ozier-Kalogiropoulos O.,  
 RA Pollenz S., Porter S., Richard G.-F., Strub M.-L., Suleau A.,  
 RA Smeenen D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,  
 RA Zentgraf M., Zivanovic Y., Bolotin-Fukuhara M., Thierri A.,  
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissendach J.,  
 RA Winkler P., Souciet J.-L.,  
 RT "Genome evolution in yeasts."  
 RL Nature 430:35-44(2004).  
 DR EMBL, CR382139, CAG90360.1; -, Genomic\_DNA.  
 DR InterPro, IPR001680, WD40.  
 DR Pfam, PF00400, WD40, 6.  
 DR SMART, SM00320, WD40, 6.  
 DR PROSITE, PS50294, WD REPEATS REGION; 1.  
 KM Complete proteome; Repeat: WD repeat.  
 SQ SEQUENCE 1048 AA; 117153 MW; 7BAEB602ACF85373 CRC64;

Query Match 48.5%; Score 50; DB 2; Length 1048;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
 Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 4 PDNAVLEGLVKYTGANG 21  
 DB 26 PDNFVIEGNLMAYTASG 43

RESULT 13  
 ID Q8G456\_BIFLO PRELIMINARY; PRT; 3172 AA.  
 AC Q8G456;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE P88.  
 GN Name=fas; OrderedLocuNames=BL1537;  
 OS Bifidobacterium longum.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
 OC Bifidobacteriaceae; Bifidobacterium.  
 OX NCBI\_TaxId=216816;  
 RN [1]  
 RP NCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=NCC 2705;  
 RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;  
 RA Schell M.A., Kamitarrou M., Snel B., Vilanova D., Berger B.,  
 RA Peesl G., Zwanen M.-C., Desiere F., Bork P., Delley M.,  
 RA Fildmore R.D., Arigoni F.,  
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation  
 RT to the human gastrointestinal tract."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
 DR EMBL, AE014295, AAN25329.1; -, Genomic\_DNA.  
 DR HSP, P25715, IMLA.  
 DR GO, GO:0005835; C:fatty acid synthase complex; IEA.  
 DR GO, GO:0004312; F:fatty-acid synthase activity; IEA.  
 DR GO, GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO, GO:0016740; F:transferase activity; IEA.  
 DR GO, GO:0006118; P:electron transport; IEA.  
 DR GO, GO:0006633; P:fatty acid biosynthesis; IEA.  
 DR GO, GO:0008152; P:metabolism; IEA.  
 DR InterPro, IPR004136, 2nprop\_dioxygen.  
 DR InterPro, IPR001227, Ac transferase.  
 DR InterPro, IPR003965, Fatty acid synth.  
 DR InterPro, IPR000794, ketoacyl synth.  
 DR InterPro, IPR002539, Maoc dehydratase.  
 DR Pfam, PF00698, Acl1\_transf\_1; 1.  
 DR Pfam, PF00109, ketoacyl-synth\_1.  
 DR Pfam, PF02801, ketoacyl-synth\_C; 1.  
 DR Pfam, PF01575, Maoc dehydratase; 1.  
 DR Pfam, PF03060, NPD\_1.

DR PRINTS; PRO1483; FASYNTHASE.  
 DR PROSITE; PS00606; B\_KETOACYL\_SYNTHASE; UNKNOWN\_1.  
 KM Complete proteome.  
 SQ SEQUENCE 3172 AA; 338131 MW; 351478B8BF20CFB CRC64;

Query Match 48.5%; Score 50; DB 2; Length 3172;  
 Best Local Similarity 50.0%; Pred. No. 4.2e+02;  
 Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 AIPDNVLEGLVKYTGANG 21  
 DB 2026 AAVDSALDAPAKVTGSNG 2045

RESULT 14  
 ID Q9HXS1\_PSEAE PRELIMINARY; PRT; 592 AA.  
 AC Q9HXS1;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Probable short-chain dehydrogenase.  
 GN OrderedLocuNames=PA3324;  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxId=287;  
 RN [1]  
 RP NCLEOTIDE SEQUENCE.  
 RC STRAIN=ATCC 15692 / PA01;  
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;  
 RA Stever C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltz L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.U., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
 RT opportunistic pathogen."  
 RL Nature 406:959-964(2000).  
 DR EMBL, AE004754, AAG06712.1; -, Genomic\_DNA.  
 DR PIR; B83231, B83231.  
 DR HSP, Q724W1, IPR9.  
 DR GO, GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO, GO:0008152; P:metabolism; IEA.  
 DR InterPro, IPR000073; A/b hydrolase.  
 DR InterPro, IPR002198; ADH\_short.  
 DR InterPro, IPR002347; Adh\_short\_C2.  
 DR InterPro, IPR000639; Epox hydrolase.  
 DR InterPro, IPR000379; Ser esters.  
 DR Pfam, PF00561, Abhydrolase\_1; 1.  
 DR Pfam, PF01066, adh\_short; 1.  
 DR PRINTS; PRO0412; EPOXYDLASE.  
 DR PRINTS; PRO0081; GDRDH.  
 DR PRINTS; PRO0080; SDRFAMILY.  
 DR PROSITE; PS00061; ADH\_SHORT; UNKNOWN\_1.  
 KM Complete proteome.  
 SQ SEQUENCE 592 AA; 65770 MW; 7EAD0096DAD0157 CRC64;

Query Match 47.6%; Score 49; DB 2; Length 592;  
 Best Local Similarity 55.6%; Pred. No. 1.1e+02;  
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 PDNAVLEGLVKYTGANG 21  
 DB 318 PDASSMNGKLVVTGAGG 335

RESULT 15  
 ID Q4ZUUS\_PSESY PRELIMINARY; PRT; 732 AA.  
 AC Q4ZUUS;  
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, last sequence update)  
 DT 13-SEP-2005 (TREMBlrel. 31, last annotation update)  
 DE Outer membrane autotransporter barrel precursor.  
 GN ORFNames=PsyT 2034;  
 OS Pseudomonas syringae pv. syringae B728a.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=205918;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B728a;  
 RG DOE Joint Genome Institute;  
 RA Chain P., Laitner F., DiBartolo G., Copeland A., Lykidis A., Trong S.,  
 RA Nolan M., Goldsman E., Thiel J., Malfatti S., Lapidus A., Deter J.C.,  
 RA Land M., Richardson P.M., Kyriades N.C., Ivanova N.,  
 RT "Comparison of two complete genome sequences of Pseudomonas syringae  
 pv. syringae B728a and pv. tomato DC3000,"  
 RT Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).  
 RL [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B728a;  
 RA Loper J.;  
 RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RL [3]  
 RN NUCLEOTIDE SEQUENCE.  
 RC STRAIN=B728a;  
 RA Fell H., Fell W.S., Lindow S.E.;  
 RT Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, CP000075; AA07077.1; -, Genomic\_DNA.  
 DR InterPro; IPR005546; Auto\_transbeta.  
 DR InterPro; IPR006315; Autotransporter.  
 DR InterPro; IPR004899; Pertactin.  
 DR InterPro; IPR003991; Pertactin\_C.  
 DR Pfam; PF03797; Autotransporter; 1.  
 DR Pfam; PF03212; Pertactin; 1.  
 DR PRINTS; PRO1484; PRYACTNPFAMLY.  
 DR TIGRFAMs; TIGR01414; autotrans\_bar1; 1.  
 KM Signal.  
 FT SIGNAL  
 SQ SEQUENCE 732 AA, 32 Potential.  
 4C355FCA478A628 CRC64;

Query Match 47.6%; Score 49; DB 2; Length 732;  
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;  
 Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 6 NAVLEGSIVKVTANGANG 21  
 DB 148 NLTLEGTSTVATANGANG 163

Search completed: March 11, 2006, 05:08:44  
 Job time : 125 secs

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DR N-PSDB; AAH74579.  
XX  
PT Designing synthetic nucleic acid sequences for improved amplification,  
PT expression in host cell, by comparing free energy of folding of a  
PT starting polynucleotide and a modified polynucleotide having a codon  
PT replacement.  
PS Claim 6; Page 66-67; 117pp; English.  
XX  
CC The present sequence represents a NADPH-dependent aldehyde reductase  
CC (AR2). The polynucleotide sequence was modified using the method of  
CC the invention. The specification describes a method for designing a  
CC synthetic polynucleotide. The method comprises providing a starting  
CC polynucleotide, determining the predicted free energy of folding per base  
CC of the polynucleotide, modifying the polynucleotide by replacing a codon  
CC with a different codon to provide a modified polynucleotide, determining  
CC free energy of folding per base of the modified polynucleotide, and  
CC comparing this with that of the original polynucleotide. The method is  
CC useful for developing nucleic acid sequences that enhance expression of  
CC the encoded protein in a heterologous host. The design and preparation of  
CC the synthetic genes are used in application of gene shuffling, directed  
CC evolution and molecular breeding methods. The method allows expression of  
CC genes from various organisms such as mammals, plants, yeast, fungi and  
CC bacteria in prokaryotic hosts, such as *Escherichia coli* and eukaryotic  
CC hosts at commercially viable levels, in particular proteins with low  
CC yield such as methionine gamma-lyase from *P. putida*. (Updated on 11-SEP-  
CC 2003 to standardise OS field)  
XX  
SQ Sequence 343 AA;  
XX  
Query Match 66.8%; Score 65.5; DB 4; Length 343;  
Best Local Similarity 88.9%; Pred. No. 0.025;  
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
XX  
QY 4 DNATL-EGSLVKTGTGANG 20  
DB 5 DNATLPEGSLVLTGTGANG 22  
XX  
RESULT 5  
AAG63563  
ID AAG63563 standard; protein; 343 AA.  
XX  
AC AAG63563;  
XX  
DT 15-OCT-2001 (first entry)  
XX  
DE Amino acid sequence of a modified NADPH-dependent aldehyde reductase.  
XX  
KW Methionine gamma-lyase; mda gene; free folding energy; gene shuffling;  
KW directed evolution; molecular breeding;  
KW NADPH-dependent aldehyde reductase.  
XX  
XX Synthetic.  
OS Sporidiobolus salmonicolor.  
XX  
XX WO200155342-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 31-JAN-2001; 2001WO-US003186.  
XX  
XX 31-JAN-2000; 2000US-00494923.  
XX  
XX 08-DEC-2000; 2000US-00734237.  
XX  
XX (BIOC-) BIOCATALYTICS INC.  
XX  
XX Rozzell DJ, Bul P, Hua L;  
XX  
XX WPI, 2001-48335/52.  
XX  
XX N-PSDB; AAH74580.  
XX  
PT Designing synthetic nucleic acid sequences for improved amplification,

PT expression in host cell, by comparing free energy of folding of a  
PT starting polynucleotide and a modified polynucleotide having a codon  
PT replacement.  
XX  
PS Claim 6; Page 67-68; 117pp; English.  
XX  
CC The present sequence represents a modified NADPH-dependent aldehyde  
CC reductase (AR2). The polynucleotide sequence was modified using the  
CC method of the invention. The specification describes a method for  
CC designing a synthetic polynucleotide. The method comprises providing a  
CC starting polynucleotide, determining the predicted free energy of folding  
CC per base of the polynucleotide, modifying the polynucleotide by replacing  
CC a codon with a different codon to provide a modified polynucleotide,  
CC determining free energy of folding per base of the modified  
CC polynucleotide, and comparing this with that of the original  
CC polynucleotide. The method is useful for developing nucleic acid  
CC sequences that enhance expression of the encoded protein in a  
CC heterologous host. The design and preparation of the synthetic genes are  
CC used in application of gene shuffling, directed evolution and molecular  
CC breeding methods. The method allows expression of genes from various  
CC organisms such as mammals, plants, yeast, fungi and bacteria in  
CC prokaryotic hosts, such as *Escherichia coli* and eukaryotic hosts at  
CC commercially viable levels, in particular proteins with low yield such as  
CC methionine gamma-lyase from *P. putida*  
XX  
SQ Sequence 343 AA;  
XX  
Query Match 66.8%; Score 65.5; DB 4; Length 343;  
Best Local Similarity 88.9%; Pred. No. 0.025;  
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
XX  
QY 4 DNATL-EGSLVKTGTGANG 20  
DB 5 DNATLPEGSLVLTGTGANG 22  
XX  
RESULT 6  
AD056196  
ID AD056196 standard; protein; 343 AA.  
XX  
AC AD056196;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Sporidiobolus salmonicolor ketoreductase, aldehyde reductase II.  
XX  
KW (R)-hydroxy ester; alpha-keto ester; ketoreductase; enzyme;  
KW aldehyde reductase II.  
XX  
OS Sporidiobolus salmonicolor.  
XX  
XX US2004101937-A1.  
XX  
XX 27-MAY-2004.  
XX  
XX 08-JUL-2003; 2003US-00616320.  
XX  
XX 10-JUL-2002; 2002US-0394761P.  
XX  
XX (MOOR/) MOORE J C.  
XX (STUR/) STURR M G.  
XX (MCLA/) MCLAUGHLIN K.  
XX (KIMJ/) KIM J.  
XX  
XX Moore JC, Sturr MG, McLaughlin K, Kim J;  
XX  
XX WPI, 2004-431257/40.  
XX  
XX preparing (R)-hydroxy ester involves adding alpha-keto ester to mixture  
XX comprising ketoreductase enzyme and non-ketoreductase enzyme components.  
XX  
XX Disclosure; SEQ ID NO 3; 10pp; English.  
XX





ID AAR96967 standard; protein; 561 AA.  
 XX AAR96967;  
 AC  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-SEP-1996 (first entry)  
 XX  
 XX Pfu DNA ligase.  
 DE  
 XX thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;  
 KM LCR; template dependent ligation.  
 XX  
 OS Pyrococcus furiosus.  
 OS  
 XX US5506137-A.  
 XX  
 XX 09-APR-1996.  
 PD  
 XX  
 XX 22-JUL-1993; 93US-00096947.  
 XX  
 XX 23-JUL-1992; 92US-00919140.  
 XX  
 XX (STRA-) STRATAGENE.  
 XX  
 XX Schoettlin WE, Mathur EJ, Marsh EJ;  
 XX  
 XX WPI; 1996-200280/20.  
 DR N-PSDB; AAT14926.  
 XX  
 XX plasmid contg. gene for thermostable DNA ligase - useful in ligase chain  
 PT reactions; stable up to 100 deg. C.  
 XX  
 XX  
 PS Claim 1; Col 29-32; 29pp; English.  
 XX  
 CC The present sequence is that of a purified thermostable DNA ligase  
 CC isolated from a hyperthermophilic marine archaebacterium, Pyrococcus  
 CC furiosus (Pfu). The Pfu DNA ligase catalyzes template dependent ligation  
 CC at temperatures of about 30-80 deg.C, and substantially retains its  
 CC catalytic ability when subjected to temperatures of 85-100 deg.C. It has  
 CC an estimated mol. wt. of 50-70 kDa. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 CC  
 CC  
 SQ Sequence 561 AA;  
 XX  
 QY  
 Query Match 49.5%; Score 48.5; DB 2; Length 561;  
 Best Local Similarity 52.6%; Pred. No. 34;  
 Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;  
 2 IPDNVLEGSIVKVTGANG 20  
 ||:|||||:|  
 Db 290 IPEKAIYVGEIYAI-GENG 307

PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 XX (ELIT-) ELITRA PHARM INC.  
 XX  
 XX Wang L, Zamudio C, Malone C, Haeelbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GD, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACA41709.  
 XX  
 XX New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 XX  
 PS Claim 25; SEQ ID NO 65763; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 CC  
 SQ Sequence 636 AA;  
 XX  
 QY  
 Query Match 49.0%; Score 48; DB 6; Length 636;  
 Best Local Similarity 54.5%; Pred. No. 49;  
 Matches 12; Conservative 1; Mismatches 5; Indels 4; Gaps 1;  
 3 PDN----AVLEGSIVKVTGANG 20  
 |||:|||||:|  
 Db 268 PDNRLMSADIECKYMTVGAGG 289

RESULT 10  
 ABU37839  
 ID ABU37839 standard; protein; 636 AA.  
 XX  
 XX ABU37839;  
 DT 19-JUN-2003 (first entry)  
 DE  
 XX Protein encoded by Prokaryotic essential gene #23366.  
 XX  
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 KM  
 XX  
 XX Neisseria meningitidis.  
 OS  
 XX  
 XX WO20027183-A2.  
 XX  
 XX 03-OCT-2002.  
 PD  
 XX  
 XX 21-MAR-2002; 2002WO-US009107.  
 XX

RESULT 11  
 ADX95802  
 ID ADX95802 standard; protein; 947 AA.  
 XX  
 XX ADX95802;  
 DT 21-APR-2005 (first entry)  
 DE  
 XX Plant full length insert polypeptide seqid 58466.  
 XX

KM plant protectant; plant growth regulator; gene therapy; plant;  
KM recombinant DNA construct; physical array; plant breeding marker;  
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KM extreme osmotic condition; pathogen tolerance; pest tolerance;  
KM galactomannan production; lignin production; plant growth regulator;  
KM yield; plant growth; plant development; seed oil; protein yield;  
KM protein content.  
XX Unidentified.  
XX OS  
XX US2004034888-A1.  
XX PD  
XX 19-FEB-2004.  
XX PF 26-APR-2003; 2003US-00425114.  
XX PR 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX XX  
XX PA (LIU/) LIU J.  
XX PA (ZHOU/) ZHOU Y.  
XX PA (KOVA/) KOVALIC D K.  
XX PA (SCRE/) SCREEN S E.  
XX PA (TABA/) TABASKA J E.  
XX PA (CAOY/) CAO Y.  
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX DR WPI; 2004-180133/17.  
XX PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX PS Claim 1; SEQ ID NO 58466; 15bp; English.  
XX XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspco.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This is the amino acid sequence of a plant full length insert  
CC polypeptide that can be used in the recombinant DNA construct of the  
CC invention.  
XX SQ Sequence 947 AA;  
QY Query Match 49.0%; Score 48; DB 8; Length 947;  
Db Best Local Similarity 55.6%; Pred. No. 78;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

3 PDNAVLEGSIVKVTGANG 20  
PPNALISASLTKVAQONG 273

RESULT 12  
ADY22708  
XX ID ADY22708 standard; protein, 965 AA.  
XX AC ADY22708;

XX XX  
DT 21-APR-2005 (first entry)  
XX XX  
DE Plant full length insert polypeptide seqid 70492.  
XX XX  
KM plant protectant; plant growth regulator; gene therapy; plant;  
KM recombinant DNA construct; physical array; plant breeding marker;  
KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KM extreme osmotic condition; pathogen tolerance; pest tolerance;  
KM growth rate; cell cycle pathway; disease resistance;  
KM galactomannan production; lignin production; plant growth regulator;  
KM yield; plant growth; plant development; seed oil; protein yield;  
KM protein content.  
XX Unidentified.  
XX OS  
XX US2004034888-A1.  
XX PN  
XX PD 19-FEB-2004.  
XX PF 26-APR-2003; 2003US-00425114.  
XX PR 06-MAY-1999; 99US-00304517.  
XX PR 05-NOV-2001; 2001US-00985678.  
XX XX  
XX PA (LIU/) LIU J.  
XX PA (ZHOU/) ZHOU Y.  
XX PA (KOVA/) KOVALIC D K.  
XX PA (SCRE/) SCREEN S E.  
XX PA (TABA/) TABASKA J E.  
XX PA (CAOY/) CAO Y.  
XX PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX DR WPI; 2004-180133/17.  
XX PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX PS Claim 1; SEQ ID NO 70492; 15bp; English.  
XX XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspco.gov/sequence.html?DocID:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This is the amino acid sequence of a plant full length insert  
CC polypeptide that can be used in the recombinant DNA construct of the  
CC invention.  
XX SQ Sequence 965 AA;  
QY Query Match 49.0%; Score 48; DB 8; Length 965;  
Db Best Local Similarity 55.6%; Pred. No. 80;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

3 PDNAVLEGSIVKVTGANG 20  
PPNALISASLTKVAQONG 291

RESULT 13  
AB069084  
ID AB069084 standard; protein; 802 AA.  
XX  
XX  
AC AB069084;  
XX  
XX 29-JUL-2004 (first entry)  
XX  
DE Pseudomonas aeruginosa polypeptide #1259.  
XX  
XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
XX  
OS Pseudomonas aeruginosa.  
XX  
XX US6551795-B1.  
XX  
PD 22-APR-2003.  
XX  
XX 18-FEB-1999; 99US-00252991.  
XX  
XX 18-FEB-1998; 98US-0074788P.  
XX  
XX 27-JUL-1998; 98US-0094190P.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Rubenfeld MJ, Nolling J, Deloughery C, Bush D;  
XX  
XX WPI: 2003-615309/58.  
XX  
XX N-PSDB; ABD02655.  
XX  
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
XX  
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of  
XX  
XX PT pathological conditions resulting from bacterial infection.  
XX  
XX  
XX Disclosure: SEQ ID NO 17830; 455bp; English.  
XX  
XX  
XX The invention relates to Pseudomonas aeruginosa polypeptides and the  
XX  
XX CC polymulectides encoding them. The sequences are useful in diagnosis and  
XX  
XX CC therapy of pathological conditions, as molecular targets for diagnostics,  
XX  
XX CC prophylaxis and treatment of pathological conditions resulting from a  
XX  
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,  
XX  
XX CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
XX  
XX CC effective antibacterial targets, as targets for antibacterial drugs,  
XX  
XX CC including anti-P. aeruginosa drugs, as templates for recombinant  
XX  
XX CC production of P. aeruginosa-derived peptides or polypeptides, as target  
XX  
XX CC components for diagnosis and/or treatment of P. aeruginosa-caused  
XX  
XX CC infection, and in detection of P. aeruginosa sequences or other sequences  
XX  
XX CC of Pseudomonas species using bioclip technology. Sequences AB067826-  
XX  
XX CC AB084336 represent P. aeruginosa polypeptides of the invention. Note: The  
XX  
XX CC sequence data for this patent did not form part of the printed  
XX  
XX CC specification but was obtained in electronic format from USPTO at  
XX  
XX CC [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html)  
XX  
XX  
XX Sequence 802 AA;  
SQ  
Query Match 48.0%; Score 47; DB 7; Length 802;  
Best Local Similarity 55.6%; Pred. No. 94;  
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;  
QY 3 PDNAVEGSLVKTGANG 20  
DB 464 PDARSMNGKLVVTGAGG 481

XX  
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.  
XX  
XX KM Pseudomonas putida.  
XX  
XX OS  
XX  
XX WO200277183-A2.  
XX  
XX  
XX 03-OCT-2002.  
XX  
XX  
XX 21-MAR-2002; 2002WO-US009107.  
XX  
XX  
XX 21-MAR-2001; 2001US-00815242.  
XX  
XX 06-SEP-2001; 2001US-00948993.  
XX  
XX 25-OCT-2001; 2001US-0342923P.  
XX  
XX 08-FEB-2002; 2002US-00072851.  
XX  
XX 06-MAR-2002; 2002US-0362699P.  
XX  
XX (ELIT-) ELITRA PHARM INC.  
XX  
XX PA  
XX  
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JM;  
XX  
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
XX  
XX N-PSDB; ACA43739.  
XX  
XX WPI: 2003-029926/02.  
XX  
XX  
XX New antisense nucleic acids, useful for identifying proteins or screening  
XX  
XX PT for homologous nucleic acids required for cellular proliferation to  
XX  
XX PT isolate candidate molecules for rational drug discovery programs.  
XX  
XX  
XX Claim 25; SEQ ID NO 67793; 1766bp; English.  
XX  
XX  
XX The invention relates to an isolated nucleic acid comprising any one of  
XX  
XX CC the 6213 antisense sequences given in the specification where expression  
XX  
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
XX  
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid  
XX  
XX CC encoding a polypeptide whose expression is inhibited by the antisense  
XX  
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
XX  
XX CC polypeptide or its fragment whose expression is inhibited by the  
XX  
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding  
XX  
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
XX  
XX CC proliferation or the activity of a gene in an operon required for  
XX  
XX CC proliferation; (7) identifying a compound that influences the activity of  
XX  
XX CC the gene product or that has an activity against a biological pathway  
XX  
XX CC required for proliferation, or that inhibits cellular proliferation; (8)  
XX  
XX CC identifying a gene required for cellular proliferation or the biological  
XX  
XX CC pathway in which a proliferation-required gene or its gene product lies  
XX  
XX CC or a gene on which the test compound that inhibits proliferation of an  
XX  
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
XX  
XX CC compound's activity; (11) a culture comprising strains in which the gene  
XX  
XX CC product is overexpressed or underexpressed; (12) determining the extent  
XX  
XX CC to which each of the strains is present in a culture or collection of  
XX  
XX CC strains; or (13) identifying the target of a compound that inhibits the  
XX  
XX CC proliferation of an organism. The antisense nucleic acids are useful for  
XX  
XX CC identifying proteins or screening for homologous nucleic acids required  
XX  
XX CC for cellular proliferation to isolate candidate molecules for rational  
XX  
XX CC drug discovery programs, or for screening homologous nucleic acids  
XX  
XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
XX  
XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
XX  
XX CC the target prokaryotic essential genes. Note: The sequence data for this  
XX  
XX CC patent did not form part of the printed specification, but was obtained  
XX  
XX CC in electronic format directly from WIPO at  
XX  
XX CC [ftp.wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences)  
XX  
XX  
XX Sequence 6310 AA;  
SQ  
Query Match 48.0%; Score 47; DB 6; Length 6310;  
Best Local Similarity 37.5%; Pred. No. 1.1e+03;  
Matches 12; Conservative 2; Mismatches 6; Indels 12; Gaps 1;  
QY 1 AIPDNVAVL-----EGSLVKTGANG 20  
DB 4440 ATPDNLILAAOGLSVSGTAEGSTIKYVGPNG 4471

Job time : 117.921 secs

RESULT 15

ABG28376  
ID ABG28376 standard; protein; 133 AA.

XX AC ABG28376;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #28367.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX KM food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN W0200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Dermanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS92563.

XX PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX PS Claim 20; SEQ ID NO 58735; 103bp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic  
CC amino acid sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 133 AA;

Query March 46.9%; Score 46; DB 4; Length 133;

Best Local Similarity 52.6%; Pred. No. 17;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

OY 1 AIPDNVLEGSIVKVTGAN 19  
| | | | |  
| | | | |  
Db 5 ACPGSKATIPGKTIVTGAN 23

Search completed: March 11, 2006, 05:02:22

```

/ TITLE OF INVENTION: Purified Thermostable Pyrococcus
/ TITLE OF INVENTION: Furiosus DNA Ligase
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennte & Edmonds
/ STREET: 2730 Sand Hill Road
/ CITY: Menlo Park
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy Disk
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/916,232
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/919,140
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8142-013
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 561 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Pyrococcus Furiosus
/ INDIVIDUAL ISOLATE: DSM #3638
/ CELL TYPE: unicellular organism
/ IMMEDIATE SOURCE:
/ LIBRARY: Pyrococcus Furiosus Genomic DNA
/ CLONE: pEM1
/ US-08-916-232-1

Query Match          49.5%; Score 48.5; DB 2; Length 561;
Best Local Similarity 52.6%; Pred. No. 7.1;
Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY      2 IPDNVLEGLVKTGANG 20
      ||:|||||:|
Db      290 IPEKAIVEGLVALI-GENG 307

RESULT 6
PCT-US93-06939-1
/ Sequence 1, Application PC/TUS9306939
/ GENERAL INFORMATION:
/ APPLICANT: Eric J. Mathur
/ APPLICANT: Edward J. Marsh
/ APPLICANT: Warren E. Schoettlin
/ TITLE OF INVENTION: Purified Thermostable
/ TITLE OF INVENTION: Pyrococcus Furiosus DNA
/ TITLE OF INVENTION: Ligase
/ NUMBER OF SEQUENCES: 17
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Limbach & Limbach
/ STREET: 2001 Ferry Building
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94111
/ COMPUTER READABLE FORM:

```

```

/ MEDIUM TYPE: Diskette, 3+ inch, 1.4 Mb storage
/ COMPUTER: IBM PC Compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WordPerfect 5.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/06939
/ FILING DATE: 19930722
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/919,140
/ FILING DATE: July 23, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: STRG 20081 USA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 433-4150
/ TELEFAX: (415) 433-8716
/ TELEX: 278356
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 561 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ ORIGINAL SOURCE:
/ ORGANISM: Pyrococcus Furiosus
/ INDIVIDUAL ISOLATE: DSM #3638
/ CELL TYPE: unicellular organism
/ IMMEDIATE SOURCE:
/ LIBRARY: Pyrococcus Furiosus Genomic DNA
/ CLONE: pEM1
/ PCT-US93-06939-1

Query Match          49.5%; Score 48.5; DB 4; Length 561;
Best Local Similarity 52.6%; Pred. No. 7.1;
Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

```

```

QY      2 IPDNVLEGLVKTGANG 20
      ||:|||||:|
Db      290 IPEKAIVEGLVALI-GENG 307

```

```

RESULT 7
US-09-252-991A-17830
/ Sequence 17830, Application US/09252991A
/ Patent No. 6551795
/ GENERAL INFORMATION:
/ APPLICANT: Marc J. Rubenfield et al.
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
/ FILE REFERENCE: 107196.136
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ PRIOR FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,768
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 17830
/ LENGTH: 802
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
/ US-09-252-991A-17830

```

```

Query Match          48.0%; Score 47; DB 2; Length 802;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      3 PDNAVLEGLVKTGANG 20
      ||:|||||:|
Db      464 PDARSMNGKLVVYTGAGG 481

```

## RESULT 8

US-09-248-796A-16593  
; Sequence 16593, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248, 796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 16593  
; LENGTH: 308  
; TYPE: PRT  
; ORGANISM: Candida albicans  
US-09-248-796A-16593

Query Match 46.9%; Score 46; DB 2; Length 308;  
Best Local Similarity 43.5%; Pred. No. 9.4;  
Matches 10; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 2 IPDNV---LEGSLVKTGANG 20  
DB 51 IPDNILDAFSLKGVASVTSSG 73

## RESULT 9

US-10-012-231A-116  
; Sequence 116, Application US/10012231A  
; Patent No. 6924355  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C23  
; CURRENT APPLICATION NUMBER: US/10/012, 231A  
; CURRENT FILING DATE: 2002-06-10  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 116  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-012-231A-116

Query Match 46.9%; Score 46; DB 2; Length 331;  
Best Local Similarity 52.6%; Pred. No. 10;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AIPDNVLEGLSVKVTGAN 19  
DB 29 ACPKATIPKTVITVGAN 47

## RESULT 10

US-10-015-389A-116  
; Sequence 116, Application US/10015389A  
; Patent No. 6936436  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C48  
; CURRENT APPLICATION NUMBER: US/10/015, 389A  
; CURRENT FILING DATE: 2002-06-25  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 116  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-015-389A-116

Query Match 46.9%; Score 46; DB 2; Length 331;  
Best Local Similarity 52.6%; Pred. No. 10;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AIPDNVLEGLSVKVTGAN 19  
DB 29 ACPKATIPKTVITVGAN 47

RESULT 11  
US-10-006-768A-116  
; Sequence 116, Application US/10006768A  
; Patent No. 6936697  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, Christopher J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C10  
; CURRENT APPLICATION NUMBER: US/10/006, 768A  
; CURRENT FILING DATE: 2002-03-05  
; NUMBER OF SEQ ID NOS: 477  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 116  
; LENGTH: 331  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-768A-116

A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-778 <K1P>  
A:Cross-references: UNIPROT:Q8UCQ3; UNIPARC:UPI00000DD19D6; GB:AE007869; PIDDN:AAK6791.1  
C:Genetics:  
A:Gene: AGR\_C\_1799  
A:Map position: Circular chromosome

Query Match	46.6%	Score 48	DB 2	Length 778
Best Local Similarity	35.0%	Pred. No. 17		
Matches	7	Conservative	9	Mismatches 4
				Indels 0
				Gaps 0

```
Qy      2 AIPDNAVLEGS LVKVTGANG 21
        |:::|:::|:::|
Db     121 ALPSGLADGTMVLLSGSNG 140
```

**RESULT 8**  
 D85608  
 hypochlorite protein 21183 [imported] - *Escherichia coli* (strain O157:H7, substrain EDLg)  
 C1:Species: *Escherichia coli*  
 C1:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
 C1:Accession: D85608; E85859  
 R1:Perera, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.V.; Davis, N.W.; Lim, A.; Dimaanta, E.; Potomousis, K.; Apodaca  
 Nature 409, 529-533, 2001  
 A1>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.  
 A1:Reference number: A85480; MUID:21074935; PMID:11206551

A1:Cross-references: UNIPROT:Q8XBP2; UNIPARC:UPI00000D07CC; GB:AE005174; NID:g12513991;  
A1:Cross-references: UNIPARC:UPI00000D07CC; GB:AE005174; NID:g12513991;  
A1:Experimental source: strain O157:H7, substrain EDJ933  
A1:Accession: E85659  
A1:Status: preliminary  
A1:Molecule type: DNA  
A1:Residues: 1-111 <ST3>  
A1:Cross-references: UNIPARC:UPI00000D07CC; GB:AE005174; NID:g12514511; PIDN:AA655737.1;  
A1:Experimental source: strain O157:H7, substrain EDJ933  
C1:Genetic9;  
A1:Gene: Z1183; Z1622

Query Match	45.64;	Score 47;	DB 2;	Length 111;
Best Local Similarity	41.28;	Pred. No. 3;		
Matches	7;	Conservative	4;	Mismatches 6;
				Indels 0;
				Gaps 0.

```
QY      4 PDNAVLEGSIVKVTGAN 20
         |||:::|
Db      28 PDNAIIQGAISSVGRN 44
```

```

RESULT 9
D90218
1st ribosomal protein L6AB [imported] - Sulfolobus solfataricus
C|Species: Sulfolobus solfataricus
C|Date: 24-May-2001 #sequence_revision 24-May-2001 #ext_change 09-Jul-2004
C|Accession: D90218
R|She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan,
Jong, I.; Jeffries, A.C.; Kozeta, C.D.; Medina, N.; Peng, J.;
Jong, I.; Ragan, A.A.; Sørensen, C.W.; Van der Oost, J.
submitted to Genbank, April 2001
A|Description: Sulfolobus solfataricus complete genome.

```

A/Accession: D90218  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-181 <KUR>

A/Cross-references: UNIPROT:Q9UX91; UNIPARC:UPI0000134165; GB:AE006641; NID:g33813871; E  
C/GeneID: 16616  
C/Superfamily: ribosomal protein L6/L9

Query Match	45.6%	Score 47;	DB 2;	Length 181;
Best Local Similarity	47.6%	Pred. No. 5.1;		
Matches 10;	Conservative 4;	Mismatches 5;	Indels 2;	Gaps 1;

```
QY      3 IPDNAY--LEGS LKVTGANG 21
          ||| :||:| |
Db     12 IPKNVVVDLKGSIIKIKGPKG 32
```

RESULT 10  
H70326  
bromothetical protein aa 294 - Amifex aeolicus

C:Species: *Aquilex aeolicus*  
C:Date: 08-May-1998 #sequence revision 08-May-1998 #text\_change 09-Jul-2004  
C:Accession: H70326  
P:Depositor: G. Warren, P. V. Gaasterland, T. Young, W. G. Lenox, A. L. Grainger

R. Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V. 2000 273 270 1000

A; Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
Nature 392, 353-358, 1998

A;Reference number: A70300; MUID:98196666; PMID:953/320  
A;Accession: H70326

A; Status: preliminary; nucleic acid sequence not shown; translation not shown  
 1; Molecule type: DNA

A/Residues: 1-371 <AQF>

A;Cross-References: UNIPROT:O68644; UNIPARC:O610000005621; GO:0000002; KEGG:05311; A;Experimental source: strain VF5

C:Genetics:  
A:Gene: aq 294

Query Match	45.6%	Score 47;	DB 2;	Length 371;
Best Local Similarity	50.0%	Pred. No. 11;		
Matches	8;	Conservative	5;	Mismatches 3;
				Indels 0;
				Gaps 0

```
QY      1 MAIPDNVLEGS LKV 16
      : ||: ||: ||: ||:
Db      319 LLIPEKAILEGN RVKI 334
```

RESULT 11  
A32687  
11v11 endopeptidase (EC 3.4.21.50) precursor - *Achromobacter lyticus* (strain M497-1)

C:\Date: 07-Sep-1990 #sequence\_ revision 07-Sep-1990 #text\_change 09-Jul-2004

C/Accession: A3268//; A32960  
R;Ohara, T.; Makino, K.; Shinagawa, H.; Nakata, A.; Norioka, S.; Sakiyama, F.

J. Biol. Chem. 264, 20625-20631, 1989  
A: Title: Cloning, nucleotide sequence, and expression of *Achromobacter* protease I gene

A; Reference number: A32687; MUID: 90062204; PMID: 2684982  
A; Accession: A32687

A; molecule type: DNA

A;Residues: 1-653 <UHA>  
A;Cross-references: UNIPROT:P15636; UNIPARC:UPI0000125C8B; GB:J05128; NID:g141803; PIDN

R. Tsunawake, S.; Masaki, T.; Hirose, M.; Soejima, M.; Sakiyama, F.  
J. Biol. Chem. 264, 3832-3839, 1989

A; Title: The primary structure and structural character  
A; Reference number: A32960; MIID: 89139439; PMID: 24929888

A;Accession: A32960

A: molecule type: protein  
A: Residues: 206-473 <TSU>

A;Cross-references: UNIPARC:UPI000011061E  
C;Comment: This protein specifically hydrolyzes lysyl peptide bonds including the Lys-P.

**C;Keywords:** hydrolase; serine proteinase  
E-1-20/Domain: signal sequence #atatus predicted <SIG>

F-21-205/Domains: #status predicted <PRO>  
F-206-483/Domains: #status experimental] <MAT>

```
F;206-4/3/Product: acnhiomobacter proteinase 1 #status experimental
F;211-421,217-285,241-263/Disulfide bonds: #status experimental
```

F;262,318,399/Active site: His, Asp, Ser #status predicted

Query Match	45.1%	Score	46.5	DB 2	Length	653
Best Local Similarity	52.4%	Pred. No.	24			

Matches 11; Conservative 4; Mismatches 5; Indels 1; Gaps 1.





Query Match 46.9%; Score 46; DB 2; Length 331;  
Best Local Similarity 52.6%; Pred. No. 10;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AIPDNVLEGSIVKVTGAN 19  
DB 29 ACPSKATIPGKTVITGAN 47

RESULT 12  
US-10-015-671A-116  
Sequence 116, Application US/10015671A

PATENT NO. 6946263  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C47  
CURRENT APPLICATION NUMBER: US/10/015,671A  
CURRENT FILING DATE: 2001-12-11  
Prior application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 116  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-015-671A-116

Query Match 46.9%; Score 46; DB 2; Length 331;  
Best Local Similarity 52.6%; Pred. No. 10;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AIPDNVLEGSIVKVTGAN 19  
DB 29 ACPSKATIPGKTVITGAN 47

RESULT 13  
US-10-015-393A-116  
Sequence 116, Application US/10015393A  
PATENT NO. 6951737  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C46  
CURRENT APPLICATION NUMBER: US/10/015,393A

CURRENT FILING DATE: 2002-06-10  
Prior application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 116  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-015-393A-116

Query Match 46.9%; Score 46; DB 2; Length 331;  
Best Local Similarity 52.6%; Pred. No. 10;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AIPDNVLEGSIVKVTGAN 19  
DB 29 ACPSKATIPGKTVITGAN 47

RESULT 14  
US-10-011-833A-116  
Sequence 116, Application US/10011833A

PATENT NO. 6951920  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2830P1C22  
CURRENT APPLICATION NUMBER: US/10/011,833A  
CURRENT FILING DATE: 2002-06-25  
Prior application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 477  
SEQ ID NO 116  
LENGTH: 331  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-011-833A-116

Query Match 46.9%; Score 46; DB 2; Length 331;  
Best Local Similarity 52.6%; Pred. No. 10;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 AIPDNVLEGSIVKVTGAN 19  
DB 29 ACPSKATIPGKTVITGAN 47

RESULT 15  
US-10-006-041A-116  
Sequence 116, Application US/10006041A  
PATENT NO. 6951921  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Baton, Dan I.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.

```

; APPLICANT: Grimaudi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C8
; CURRENT APPLICATION NUMBER: US/10/006,041A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 116
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-006-041A-116

```

```

Query Match      46.9%; Score 46; DB 2; Length 331;
Best Local Similarity 52.6%; Pred. No. 10;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1 AIPDNAVLESGLVKVTGAN 19
Db      29 ACPKATIPGKTVIVTGAN 47

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Search completed: March 11, 2006, 05:11:13  
 Job time : 28.3016 secs

```
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32256
LENGTH: 388
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(388)
OTHER INFORMATION: Ceres Seq. ID no. 13592517
US-11-096-568A-32256

Query Match          41.3%; Score 42.5; DB 7; Length 388;
Best Local Similarity 28.9%; Pred. No. 29;
Matches 11; Conservative 4; Mismatches 2; Indels 21; Gaps 1;

Qy      4 PDNAVLEGSIV-----KVTGAN 20
Db      160 PDVCVDSGLTYATYEGHPFIQLFVKALGSKITGAN 197

RESULT 8
US-11-096-568A-20894
Sequence 20894, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20894
LENGTH: 210
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(210)
OTHER INFORMATION: Ceres Seq. ID no. 12390165
US-11-096-568A-20894

Query Match          40.8%; Score 42; DB 7; Length 210;
Best Local Similarity 57.1%; Pred. No. 17;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AIPDNVLEGSIVK 15
Db      108 ALPDTSVLRGTLOK 121

RESULT 9
US-11-096-568A-20893
Sequence 20893, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20893
LENGTH: 277
```

```
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(277)
OTHER INFORMATION: Ceres Seq. ID no. 12390164
US-11-096-568A-20893

Query Match          40.8%; Score 42; DB 7; Length 277;
Best Local Similarity 57.1%; Pred. No. 23;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      2 AIPDNVLEGSIVK 15
Db      175 ALPDTSVLRGTLOK 188

RESULT 10
US-11-096-568A-1267
Sequence 1267, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1267
LENGTH: 246
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(246)
OTHER INFORMATION: Ceres Seq. ID no. 13624403
US-11-096-568A-1267

Query Match          40.3%; Score 41.5; DB 7; Length 246;
Best Local Similarity 57.9%; Pred. No. 24;
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy      4 PDNAVLEGSIVKVTGAN 21
Db      221 PRAVAVLQSQDEKALGANG 239

RESULT 11
US-11-096-568A-1266
Sequence 1266, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Theby
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1266
LENGTH: 283
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(283)
OTHER INFORMATION: Ceres Seq. ID no. 13624402
US-11-096-568A-1266

Query Match          40.3%; Score 41.5; DB 7; Length 283;
Best Local Similarity 57.9%; Pred. No. 29;
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
```

Qy 4 PDNAV-LEGS L V K T G A N G 21  
Db 258 PKRAVLLQGSQE K A L G A N G 27

```

RESULT 12
US-11-096-568A-1265
: Sequence 1265, Application US/11096568A
: Publication No. US20060048240A1
: GENERAL INFORMATION:
: APPLICANT: Alexandrov, Nickolai et al.
: TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
: TITLE OF INVENTION: Theory
: FILE REFERENCE: 2750-1592PUS2
: CURRENT APPLICATION NUMBER: US/11/096,568A
: CURRENT FILING DATE: 2005-04-01
: NUMBER OF SEQ ID NOS: 34471
: SEQ ID NO 1265
: LENGTH: 316
: TYPE: PRT
: ORGANISM: Zea mays subsp. mays
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)..(316)
: OTHER INFORMATION: Ceres Seq. ID no. 13624401
: US-11-096-568A-1265

```

Query Match Similarity 40.3%; Score 41.5; DB 7; Length 316;  
Best Local Similarity 57.9%; Pred. No. 33;  
Matches 11; Conservative 6; Indels 1; Gaps 1.

```
Qy      4 PDNAV-LEGSIVKVTGANG 21
         | | | | |
Db      291 PKRAVLQGSQEKALGANG 309
```

```

RESULT 13
US-11-052-554A-211
Sequence 211, Application US/11052554A
Publication No. US2005028886A1
GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PatentIn version 3.3
SEQ ID NO 211
LENGTH: 1562
TYPE: PRT
ORGANISM: Streptococcus mutans UA159
US-11-052-554A-211

```

Query Match	40.3%	Score	41.5	DB	7	Length	1562
Best Local Similarity	52.6%	Pred.	No. 2.3e+02				
Matches	10	Conservative	3	Mismatches	5	Indels	1
						Gaps	1

QY	4	PDNAV-LEGLSVKVTGANG	21
		:   :	
Db	1210	PEEALRQDLVKITDANG	1228

RESULT 14  
US-11-087-099-4990  
; Sequence 4990, Application US/11087099  
; Publication No. US20060041961A1

```

: GENERAL INFORMATION:
: APPLICANT: Abad, Mark S. et al.
: TITLE OR INVENTION: Genes and Uses for Plant Improvement
: FILE REFERENCE: 38-21(53450)B EP
: CURRENT APPLICATION NUMBER: US/11/087,099
: CURRENT FILING DATE: 2005-03-22
: NUMBER OF SEQ ID NOS: 12464
: SEQ ID NO 4990
: LENGTH: 175
: TYPE: prt
: ORGANISM: Brucella melitensis 16M
: US-11-087-099-4990

```

Query March	39.8%	Score 41	DB 7	Length 175
Best Local Similarity	50.0%	Pred. No. 19		
Matches 8	Conservative 4	Mismatches 4	Indels 0	Gaps 0

```
Qy      1 MAIPDNVLEGS LKV 16
          ||||::||:|
Db      127 MEIPDNSLVGSPARV 142
```

```

RESULT 15
US-11-096-568A-12932
: Sequence 12932, Application US/11096568A
: Publication NO. US20060048240A1
: GENERAL INFORMATION:
: APPLICANT: Alexandrov, Nikolai et al.
: TITLE OF INVENTION: Sequence-Determined DNA Fr
: FILE REFERENCE: 2750-1592PUS2
: CURRENT APPLICATION NUMBER: US/11/096,568A
: CURRENT FILING DATE: 2005-04-01
: NUMBER OF SEQ ID NOS: 34471
: SEQ ID NO 12932
: LENGTH: 234
: TYPE: PR1
: ORGANISM: Triticum aestivum
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)-(234)
: OTHER INFORMATION: Cereals Seq. ID no. 1431384
US-11-096-568A-12932

```

Query March	39.8%	Score 41;	DB 7;	Length 234;
Best Local Similarity	50.0%	Pred. No. 27;		
Matches 8; Conservative	3;	Mismatches 5;	Indels 0;	Gaps 0;

```
QY      4 PDNAVLEGS LVKVTGA 19
      || :|::||| ||
Db      71 PDGFCIESNVVKVLGA 86
```

Search completed: March 11, 2006, 05:16:53  
Job time : 12.3333 secs

```

; APPLICANT: Bul, Peter
; APPLICANT: Hua, Ling
; TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
; FILE REFERENCE: B583:53896
; CURRENT APPLICATION NUMBER: US/10/989,488A
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 09/494,921
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/734,237
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 35
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Sporidiobolus salmonicolor
; US-10-989-488A-35

```

```

Query Match      66.5%; Score 68.5; DB 5; Length 343;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 18; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```

```

Qy      1 MAIPDNAVLEGSIVKVTGANG 21
Db      1 MAKIDNAVLEPGSLVLTGTGANG 22

```

```

RESULT 8
US-10-989-488A-37
; Sequence 37, Application US/10989488A
; Publication No. US20050196774A1
; GENERAL INFORMATION:
; APPLICANT: Rozzell, J. David
; APPLICANT: Bul, Peter
; APPLICANT: Hua, Ling
; TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION
; FILE REFERENCE: B583:53896
; CURRENT APPLICATION NUMBER: US/10/989,488A
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 09/494,921
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 09/734,237
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 37
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic protein derived from Sporidiobolus salmonicolor
; OTHER INFORMATION: NADPH-Dependent Aldehyde Reductase 2, having an ala to gly
; OTHER INFORMATION: mutation at amino acid position 2
; US-10-989-488A-37

```

```

Query Match      66.5%; Score 68.5; DB 5; Length 343;
Best Local Similarity 81.8%; Pred. No. 0.011;
Matches 18; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```

```

Qy      1 MAIPDNAVLEGSIVKVTGANG 21
Db      1 MAKIDNAVLEPGSLVLTGTGANG 22

```

```

RESULT 9
US-10-437-963-171580
; Sequence 171580, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```

```

; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171580
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6979C.1.dep
; US-10-437-963-171580

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Query Match      49.5%; Score 51; DB 4; Length 279;
Best Local Similarity 62.5%; Pred. No. 6.9;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      5 DNAVEGSLVKTGTAN 20
Db      71 DSPILVGSIAKTGTGN 86

```

```

RESULT 10
US-10-282-122A-65763
; Sequence 65763, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forey, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 65763
; LENGTH: 636

```

TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-10-282-122A-65763

Query Match 46.6%; Score 48; DB 4; Length 636;  
Best Local Similarity 54.5%; Pred. No. 58;  
Matches 12; Conservative 1; Mismatches 5; Indels 4; Gaps 1;

QY 4 PDNAVLEGSIVKVTGANG 21  
DB 268 PPNRLMSADIEGKTWVTGAGG 289

## RESULT 11

US-10-425-115-273937  
Sequence 273937, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ. ID NOS: 369326  
SEQ. ID NO 273937  
LENGTH: 892  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(892)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_181416C.1.pep  
US-10-425-115-273937

Query Match 46.6%; Score 48; DB 4; Length 892;  
Best Local Similarity 55.6%; Pred. No. 88;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 PDNAVLEGSIVKVTGANG 21  
DB 202 PPNALLSASLTKVAQONG 219

## RESULT 12

US-10-425-114-58466  
Sequence 58466, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53113)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ. ID NOS: 73128  
SEQ. ID NO 58466  
LENGTH: 947  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: 700363178\_FLI.pep  
US-10-425-114-58466

Query Match 46.6%; Score 48; DB 4; Length 947;  
Best Local Similarity 55.6%; Pred. No. 94;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 PDNAVLEGSIVKVTGANG 21  
DB 256 PPNALLSASLTKVAQONG 273

## RESULT 13

US-10-425-114-70492  
Sequence 70492, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ. ID NOS: 73128  
SEQ. ID NO 70492  
LENGTH: 965  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: UC-ZMFLB73025E08\_FLI.pep  
US-10-425-114-70492

Query Match 46.6%; Score 48; DB 4; Length 965;  
Best Local Similarity 55.6%; Pred. No. 96;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 PDNAVLEGSIVKVTGANG 21  
DB 274 PPNALLSASLTKVAQONG 291

## RESULT 14

US-10-282-122A-67793  
Sequence 67793, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Cart, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forey, R.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITPA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06

Search completed: March 11, 2006, 05:16:12  
Job time : 97.3333 secs

PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: Patentin version 3.1  
SEQ ID NO: 67793  
LENGTH: 6310  
TYPE: PRT  
ORGANISM: Pseudomonas putida  
US-10-282-122A-67793

Query Match 45.6%; Score 47; DB 4; Length 6310;  
Best Local Similarity 37.5%; Pred. No. 1.3e+03;  
Matches 12; Conservative 2; Mismatches 6; Indels 12; Gaps 1;

QY 2 AIPDNNAV-----BGSIVKYTGANG 21  
DB 4440 ATPDNLILADLSVSGTAAGSTIKYVGPNG 4471

RESULT 15  
US-10-450-763-58735  
Sequence 58735, Application US/10450763  
Publication No. US20050196754A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP3/US  
CURRENT APPLICATION NUMBER: US/10/450,763  
CURRENT FILING DATE: 2003-06-11  
PRIOR APPLICATION NUMBER: PCT/US01/08631  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
NUMBER OF SEQ ID NOS: 60736  
SOFTWARE: Custom  
SEQ ID NO: 58735  
LENGTH: 133  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (92)..(104)  
OTHER INFORMATION: GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE domain  
OTHER INFORMATION: identified by eMATRIX, accession number PR00081B, p-value=6.727e-  
OTHER INFORMATION: 11, raw score of 10.38  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (15)..(131)  
OTHER INFORMATION: short chain dehydrogenase domain identified by Pfam,  
OTHER INFORMATION: accession name adh\_short, E-value=9.1e-05, Pfam score of -12.5  
US-10-450-763-58735

Query Match 44.7%; Score 46; DB 5; Length 133;  
Best Local Similarity 52.6%; Pred. No. 19;  
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 AIPDNNAVLEGSIVKYTGANG 20  
DB 5 ACPSKATIPKTYIVTGAN 23

**This Page Blank (uspto)**



```

TITLE OF INVENTION: Purified Thermostable Pyrococcus
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,232
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/919,140
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8142-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 561 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: Pyrococcus Furiosus
INDIVIDUAL ISOLATE: DSM #3638
CELL TYPE: unicellular organism
IMMEDIATE SOURCE:
LIBRARY: Pyrococcus Furiosus Genomic DNA
CLONE: PEM1
US-08-916-232-1

Query Match      47.1%; Score 48.5; DB 2; Length 561;
Best Local Similarity 52.6%; Pred. No. 7.7;
Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1

QY          3 IPDNAVLEGSLVKTGTANG 21
||:|::|::|::|: ||
Db          290 IPEKAIVEGELVALI-GENG 307

RESULT 6
PCT-US93-06939-1
Sequence 1, Application PC/TUS9306939
GENERAL INFORMATION:
APPLICANT: Eric J. Mathur
APPLICANT: Edward J. Marsh
APPLICANT: Warren E. Schoettlin
TITLE OF INVENTION: Purified Thermostable
TITLE OF INVENTION: Pyrococcus Furiosus DNA
TITLE OF INVENTION: Ligase
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Limbach & Limbach
STREET: 2001 Perry Building
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:

```

MEDIUM TYPE: Diskette, 3+ inch, 1.4 MB storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Wordperfect 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US93/06939  
FILING DATE: 19930722

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/919,140  
FILING DATE: July 23, 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Albert P. Halluin  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: STRG 20081 USA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 433-4150  
TELEFAX: (415) 433-8716  
TELEX: 278356

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 561 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
ORIGINAL SOURCE:  
ORGANISM: Pyrococcus Furiosus  
INDIVIDUAL ISOLATE: DSM #3638  
CELL TYPE: unicellular organism  
IMMEDIATE SOURCE:  
LIBRARY: Pyrococcus Genomic DNA  
CLONE: pEM1

PCT-US93-06939-1

Query Match 47.1%; Score 48.5; DB 4; Length 561;  
Best Local Similarity 52.6%; Pred. No. 7.7;  
Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

OY 3 IPDNAVLEGSLLVKTGANG 21  
|||:::|||::|||  
Db 290 IPEKAIIVEGLVALI-GENG 307

RESULT 7  
US-09-252-991A-17830  
Sequence 17830, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 17830  
LENGTH: 802  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17830

Query Match 45.6%; Score 47; DB 2; Length 802;  
Best Local Similarity 55.6%; Pred. No. 21;  
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

OY 4 PDNAVLEGSLLVKTGANG 21  
|||:::|||::|||  
Db 464 PDARSMNGKLIVVTGAG 481

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RESULT 8
US-08-849-602C-27
; Sequence 27, Application US/08849602C
; Patent No. 6171823
; GENERAL INFORMATION:
; APPLICANT: Fabricius, Heile
; APPLICANT: Hascrup, Sven
; TITLE OF INVENTION: A Process of Producing
; TITLE OF INVENTION: Extracellular Proteins in Bacteria
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESSSEE: No. 61718230 No. 6171823disk of No. 6171823th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PatSeq for windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/849,602C
; FILING DATE: 02-JUN-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 4139, 204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 653 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-849-602C-27

Query Match 45.1%; Score 46.5; DB 2; Length 653;
Best Local Similarity 52.4%; Pred. No. 20;
Matches 11; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 MAIPDNVLEGSIVKVTGANG 21
Db 568 VAIPDNATVE-SPIVSGRTG 587

RESULT 9
5248599-2
; Patent No. 5248599
; APPLICANT: SAKIYAMA, FUMIO; NAKATA, ATSUC
; TITLE OF INVENTION: ACHROMOBACTER PROTEASE I GENE AND GENE
; PRODUCT THEREOF
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/482,266
; FILING DATE: 20-FEB-1990
; SEQ ID NO: 2:
; LENGTH: 653
; 5248599-2

Query Match 45.1%; Score 46.5; DB 6; Length 653;
Best Local Similarity 52.4%; Pred. No. 20;
Matches 11; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

QY 1 MAIPDNVLEGSIVKVTGANG 21
Db 568 VAIPDNATVE-SPIVSGRTG 587
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RESULT 10
US-09-248-796A-16593
; Sequence 16593, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16593
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-16593
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Query Match 44.7%; Score 46; DB 2; Length 308;
Best Local Similarity 43.5%; Pred. No. 10;
Matches 10; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 3 IPDNV---LEGSIVKVTGANG 21
Db 51 IPNIDAFSLKGVASVYTGSSG 73
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RESULT 11
US-10-012-231A-116
; Sequence 116, Application US/10012231A
; Patent No. 6924355
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Denoyers, Luc
; APPLICANT: Baton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830PIC23
; CURRENT APPLICATION NUMBER: US/10/012,231A
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 116
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-012-231A-116
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Query Match 44.7%; Score 46; DB 2; Length 331;
Best Local Similarity 52.6%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 AIPDNVLEGSIVKVTGAN 20
Db 29 ACPSKATIPGKTVIVTGAN 47
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```
RESULT 12
US-10-015-389A-116
Sequence 116 Application US/10015389A
Patent No. 6936436
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC48
CURRENT APPLICATION NUMBER: US/10/015.389A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-10-015-389A-116

Query Match          44.7%; Score 46; DB 2; Length 331;
Best Local Similarity 52.6%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      2 AIPDNVLEGSIVKVTGAN 20
DB      29 ACPSKATIPGKIVITGAN 47

RESULT 13
US-10-006-768A-116
Sequence 116 Application US/10006768A
Patent No. 6936897
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC10
CURRENT APPLICATION NUMBER: US/10/006.768A
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 477
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-10-006-768A-116
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Query Match          44.7%; Score 46; DB 2; Length 331;
Best Local Similarity 52.6%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      2 AIPDNVLEGSIVKVTGAN 20
DB      29 ACPSKATIPGKIVITGAN 47

RESULT 14
US-10-015-671A-116
Sequence 116 Application US/10015671A
Patent No. 6946263
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC47
CURRENT APPLICATION NUMBER: US/10/015.671A
CURRENT FILING DATE: 2001-12-11
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 116
LENGTH: 331
TYPE: PRT
ORGANISM: Homo sapiens
US-10-015-671A-116

Query Match          44.7%; Score 46; DB 2; Length 331;
Best Local Similarity 52.6%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      2 AIPDNVLEGSIVKVTGAN 20
DB      29 ACPSKATIPGKIVITGAN 47

RESULT 15
US-10-015-393A-116
Sequence 116 Application US/10015393A
Patent No. 6951737
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Guiney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PIC46
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: CURRENT APPLICATION NUMBER: US/10/015.393A
: CURRENT FILING DATE: 2002-06-10
: Prior Application removed - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 477
: SEQ ID NO 116
: LENGTH: 331
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-015-393A-116
    
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Query Match 44.7%; Score 46; DB 2; Length 331;
Best Local Similarity 52.6%; Pred. No. 11;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
    
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QY 2 AIPDNATLESLVKTGAN 20
Db 29 ACPSKATTPGKTVIVTGAN 47
    
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Search completed: March 11, 2006, 05:11:14
Job time : 28.6667 secs
    
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ID AAR96967 standard; protein; 561 AA.  
 XX  
 AC AAR96967;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-SEP-1996 (first entry)  
 XX  
 DE Pfu DNA ligase.  
 KM thermostable ligase; Pfu; Pyrococcus furiosus; ligase chain reaction;  
 KM LCR; template dependent ligation.  
 XX  
 OS Pyrococcus furiosus.  
 XX  
 PN US5506137-A.  
 PD 09-APR-1996.  
 XX  
 PP 22-JUL-1993; 93US-00096947.  
 XX  
 PR 23-JUL-1992; 92US-00919140.  
 XX  
 PA (STRA-) STRATAGENE.  
 XX  
 PI Schoettlin WE, Mathur EJ, Marsh EJ;  
 XX  
 DR WPI; 1996-200280/20.  
 DR N-PSDB; AAT14926.  
 PT plasmid contg. gene for thermostable DNA ligase - useful in ligase chain  
 PT reactions, stable up to 100 deg. C.  
 XX  
 PS Claim 1; Col 29-32; 29pp; English.  
 XX  
 CC The present sequence is that of a purified thermostable DNA ligase  
 CC isolated from a hyperthermophilic marine archaeobacterium, Pyrococcus  
 CC furiosus (Pfu). The Pfu DNA ligase catalyses template dependent ligation  
 CC at temperatures of about 30-80 deg.C, and substantially retains its  
 CC catalytic ability when subjected to temperatures of 85-100 deg.C. It has  
 CC an estimated mol. wt. of 50-70 kDa. (Updated on 25-MAR-2003 to correct PF  
 CC field.)  
 CC  
 SQ Sequence 561 AA;  
 SQ  
 Query Match 47.1%; Score 48.5; DB 2; Length 561;  
 Best Local Similarity 52.6%; Pred. No. 38;  
 Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;  
 OY 3 IPDNVLEGSGLVKVTGANG 21  
 ||:|||||:|  
 DB 290 IPEKAIIVEGELVAI-GENG 307  
 RESULT 10  
 ABU37839  
 ID ABU37839 standard; protein; 636 AA.  
 XX  
 AC ABU37839;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Protein encoded by Prokaryotic essential gene #23366.  
 KM  
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN WO20027183-A2.  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX

PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948893.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haeselbeck R, Ohlsen KL, Zyskind JW;  
 PI Wall D, Trawick JD, Carr GD, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 DR N-PSDB; ACRA1709.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 25; SEQ ID NO 65763; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 CC  
 SQ Sequence 636 AA;  
 SQ  
 Query Match 46.6%; Score 48; DB 6; Length 636;  
 Best Local Similarity 54.5%; Pred. No. 54;  
 Matches 12; Conservative 1; Mismatches 5; Indels 4; Gaps 1;  
 OY 4 PDN----AVLEGSGLVKVTGANG 21  
 |||:|||||  
 DB 268 PDNRLMSADIEGKYVWTGAGS 289  
 RESULT 11  
 ADX95802  
 ID ADX95802 standard; protein; 947 AA.  
 XX  
 AC ADX95802;  
 XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Plant full length insert polypeptide seqid 58466.  
 XX

KM plant protectant; plant growth regulant; gene therapy; plant;  
 KM recombinant DNA construct; physical array; plant breeding marker;  
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KM growth rate; cell cycle pathway; disease resistance;  
 KM galactomannan production; lignin production; plant growth regulator;  
 KM yield; plant growth; plant development; seed oil; protein yield;  
 KM protein content.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004034888-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 28-APR-2003; 2003US-00425114.  
 XX  
 PR 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX  
 PA (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX  
 DR WPI; 2004-180133/17.  
 XX  
 PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 PS  
 PS Claim 1; SEQ ID NO 58466; 15pp; English.  
 XX  
 CC The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.secdeta.uspo.gov/sequence.html?docID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX  
 SQ Sequence 947 AA;  
 Query Match 46.6%; Score 48; DB 8; Length 947;  
 Best Local Similarity 55.6%; Pred. No. 86;  
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 4 PDNAVLEGSIVKVTGANG 21  
 Db PPNALUSASLTKVAQONG 273  
 RESULT 12  
 ADY22708  
 ID ADY22708 standard; protein, 965 AA.  
 XX  
 AC ADY22708;

XX  
 DT 21-APR-2005 (first entry)  
 XX  
 DE Plant full length insert polypeptide seqid 70492.  
 XX  
 KM plant protectant; plant growth regulant; gene therapy; plant;  
 KM recombinant DNA construct; physical array; plant breeding marker;  
 KM cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
 KM extreme osmotic condition; pathogen tolerance; pest tolerance;  
 KM growth rate; cell cycle pathway; disease resistance;  
 KM galactomannan production; lignin production; plant growth regulator;  
 KM yield; plant growth; plant development; seed oil; protein yield;  
 KM protein content.  
 XX  
 OS Unidentified.  
 XX  
 PN US2004034888-A1.  
 XX  
 PD 19-FEB-2004.  
 XX  
 PF 28-APR-2003; 2003US-00425114.  
 XX  
 PR 06-MAY-1999; 99US-00304517.  
 PR 05-NOV-2001; 2001US-00985678.  
 XX  
 PA (LIU/) LIU J.  
 PA (ZHOU/) ZHOU Y.  
 PA (KOVA/) KOVALIC D K.  
 PA (SCRE/) SCREEN S E.  
 PA (TABA/) TABASKA J E.  
 PA (CAOY/) CAO Y.  
 XX  
 PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
 XX  
 DR WPI; 2004-180133/17.  
 XX  
 PT New recombinant DNA construct, useful for improving plant tolerance to  
 PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
 PT pests, for conferring increased resistance to plant disease, or for  
 PT improving yield.  
 PS  
 PS Claim 1; SEQ ID NO 70492; 15pp; English.  
 XX  
 CC The invention describes a recombinant DNA construct comprising a  
 CC polynucleotide consisting of a sequence encoding an amino acid sequence  
 CC available in electronic form from the US patent office at  
 CC ftp.secdeta.uspo.gov/sequence.html?docID:2004034888. The polynucleotide  
 CC of the invention are also useful in physical arrays of molecules and as  
 CC plant breeding markers. The recombinant DNA construct is useful for  
 CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
 CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
 CC plant cells by modification of the cell cycle pathway, for conferring  
 CC increased resistance to plant disease, for producing galactomannan,  
 CC lignin or plant growth regulators, for increasing the rate of homologous  
 CC recombination in plants, for improving yield by modification of  
 CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
 CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This is the amino acid sequence of a plant full length insert  
 CC polypeptide that can be used in the recombinant DNA construct of the  
 CC invention.  
 XX  
 SQ Sequence 965 AA;  
 Query Match 46.6%; Score 48; DB 8; Length 965;  
 Best Local Similarity 55.6%; Pred. No. 88;  
 Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 4 PDNAVLEGSIVKVTGANG 21  
 Db PPNALUSASLTKVAQONG 291



XX	ADY65680	ADY65680 standard; protein; 272 AA.
XX	ADY65680	
AC	ADY65680	
XX	02-JUN-2005	(first entry)
DT	02-JUN-2005	
XX	S. mansoni	protein SEQ ID 1098.
DE	S. mansoni	protein SEQ ID 1098.
XX	Schistosomacide; schistosomiasis; psychiatric disorder; vaccine;	
KW	Schistosomacide; schistosomiasis; psychiatric disorder; vaccine;	
XX	Schistosomacide; schistosomiasis; psychiatric disorder; vaccine;	
XX	Schistosoma mansoni.	
OS	Schistosoma mansoni.	
XX	W02005023979-A2.	
PN	W02005023979-A2.	
XX	17-MAR-2005.	
PD	17-MAR-2005.	
XX	10-SEP-2004; 2004WO-BR000170.	
PF	10-SEP-2004; 2004WO-BR000170.	
XX	11-SEP-2003; 2003US-0502277P.	
PR	11-SEP-2003; 2003US-0502277P.	
XX	(AMPA-) FUNDAÇÃO AMPARO À PESQUISA DO ESTADO.	
PA	(AMPA-) FUNDAÇÃO AMPARO À PESQUISA DO ESTADO.	
XX	Verjovsky-Almeida S, Leite LCC, Farias LP, Miyasato PA, Kawano T;	
PI	Verjovsky-Almeida S, Leite LCC, Farias LP, Miyasato PA, Kawano T;	
PI	Demarco R, Garcia JCL, Martins EAL, Ho PL, Nascimento ALTO;	
PI	Dias-Neto E, Secubal JC, Menck CFM, Madeira AMEN, Rodrigues V;	
PI	Gargioni C;	
XX	WPI; 2005-223357/23.	
DR	WPI; 2005-223357/23.	
XX	New isolated nucleic acid molecule encoding a Schistosoma mansoni	
PT	protein, useful for as a vaccine or for preventing, diagnosing, or	
PT	treating Schistosoma mansoni infection.	
XX	treating Schistosoma mansoni infection.	
XX	treating Schistosoma mansoni infection.	
PS	treating Schistosoma mansoni infection.	
XX	Disclosure; SEQ ID NO 1098; 52pp; English.	
XX	Disclosure; SEQ ID NO 1098; 52pp; English.	
XX	Disclosure; SEQ ID NO 1098; 52pp; English.	
CC	The invention relates to an isolated nucleic acid molecule encoding a	
CC	Schistosoma mansoni protein, or its portion which is at least 20 amino	
CC	acids in length. Also included are an expression vector comprising the	
CC	nucleic acid operably linked to a promoter, a recombinant cell	
CC	transformed/transfected with the nucleic acid (or expression vector), an	
CC	immunogenic composition comprising the nucleic acid in combination with a	
CC	pharmaceutical adjuvant or carrier, an isolated S. mansoni protein	
CC	comprising an amino acid sequence encoded by the nucleic acid, an	
CC	immunogenic composition comprising the isolated S. mansoni protein, an	
CC	isolated antibody which specifically binds to the isolated S. mansoni	
CC	protein, a hybridoma cell line which produces the isolated antibody, a	
CC	method for determining a S. mansoni infection in a subject and a computer	
CC	readable medium having recorded in it a nucleic acid molecule from S.	
CC	mansoni genome. The nucleic acid molecule is useful for preventing,	
CC	diagnosing, or treating S. mansoni infection (schistosomiasis). It can	
CC	also be used as vaccine against S. mansoni. The present sequence is a	
CC	Schistosoma mansoni protein of the invention. Note: The sequence data for	
CC	this patent did not form part of the printed specification, but was	
CC	obtained in electronic format directly from WIP0 at	
CC	ftp.wipo.int/pub/published_pct_sequences. Also, SEQ ID 2141-2152 are	
CC	mentioned in the specification but are not included in the sequence	
CC	listing.	
XX	Sequence 272 AA;	
5Q	Sequence 272 AA;	

Query Match	45.6%	Score 47	DB 9	Length 272	
Best Local Similarity	47.6%	Pred. No. 29			
Matches	10	Conservative	4	Mismatches	7
				Indels	0
				Gaps	0
Qy	1	MAIPDNAVEGSLVKVTGANG	21		
	:		:		:
Db	140	LAIPDLAKSGIVNVSVCG	160		
RESULT	14				

```

AB069084
ID   AB069084 standard; protein; 802 AA.
XX
XX
AC   AB069084;
XX
DT   29-JUL-2004 (first entry)
XX
DE   Pseudomonas aeruginosa polypeptide #1259.
XX
XX   Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
XX   Pseudomonas aeruginosa.
XX
OS   US6551795-B1.
XX
PN   22-APR-2003.
XX
PF   18-FEB-1999; 99US-00252991.
XX
PR   18-FEB-1998; 98US-0074788P.
XX
PR   27-JUL-1998; 98US-0094190P.
XX
PA   (GENO-) GENOME THERAPEUTICS CORP.
XX
XX
PI   Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX   WPI; 2003-615309/58.
XX
DR   N-PSDB; ABD02655.
XX
PT   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT   useful as molecular targets for diagnostics, prophylaxis and treatment of
PT   pathological conditions resulting from bacterial infection.
XX
XX
PS   Disclosure; SEQ ID NO 17830; 455BP; English.
XX
XX
CC   The invention relates to Pseudomonas aeruginosa polypeptides and the
CC   polynucleotides encoding them. The sequences are useful in diagnosis and
CC   therapy of pathological conditions, as molecular targets for diagnostics,
CC   prophylaxis and treatment of pathological conditions resulting from a
CC   bacterial infection, for evaluating a compound, such as a polypeptide,
CC   for the ability to bind a P. aeruginosa nucleic acid, as components of
CC   effective antibacterial targets, as targets for antibacterial drugs,
CC   including anti-P. aeruginosa drugs, as templates for recombinant
CC   production of P. aeruginosa-derived peptides or polypeptides, as target
CC   components for diagnosis and/or treatment of P. aeruginosa-caused
CC   infection, and in detection of P. aeruginosa sequences or other sequences
CC   of Pseudomonas species using biotech technology. Sequences ABO67826-
CC   ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC   sequence data for this patent did not form part of the printed
CC   specification but was obtained in electronic format from USPTO at
CC   seqdata.uspto.gov/sequence.html
XX
XX
SQ   Sequence 802 AA;
XX
XX
Query Match          45.6%; Score 47; DB 7; Length 802;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0
XX
QY      4 PDNAVTEGSLVYKVTGANG 21
      |||::|||
DB      464 PDARSMNGKLVVYTGAGG 481
XX
RESULT 15
ABU39869
ID   ABU39869 standard; protein; 6310 AA.
XX
XX
AC   ABU39869;
XX
DT   19-JUN-2003 (first entry)
XX
XX
DE   Protein encoded by Prokaryotic essential gene #25396.
XX

```

Search completed: March 11, 2006, 05:02:25  
 Job time : 120.667 secs

KM Antisense; prokaryotic essential gene; cell proliferation; drug design.  
 OS Pseudomonas putida.  
 XX  
 XX WO200277183-A2.  
 PN  
 XX  
 XX 03-OCT-2002.  
 PD  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 XX (ELIT-) ELITRA PHARM INC.  
 XX  
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;  
 XX  
 XX WPI; 2003-029926/02.  
 DR N-PSDB; ACA45739.  
 XX  
 XX New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 XX  
 PS Claim 25; SEQ ID NO 67793; 1766bp; English.  
 XX  
 XX The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation or the activity of a gene in an operon required for  
 CC proliferation; (7) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,  
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of  
 CC the target prokaryotic essential genes. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 XX Sequence 6310 AA:  
 SQ  
 Query Match 45.6%; Score 47; DB 6; Length 6310;  
 Best Local Similarity 37.5%; Pred. No. 1.2e+03;  
 Matches 12; Conservative 2; Mismatches 6; Indels 12; Gaps 1;  
 QY 2 AIPDNATL-----EGSLVKVTGANG 21  
 DB 4440 ATPDNLILAADGLSVSGTAENGSTTKYGPNG 4471

APPLICANT: Bui, Peter  
APPLICANT: Hua, Ling  
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION  
FILE REFERENCE: B583:53896  
CURRENT APPLICATION NUMBER: US/10/989,488A  
CURRENT FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: 09/494,921  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 09/734,237  
PRIOR FILING DATE: 2000-12-08  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 35  
LENGTH: 343  
TYPE: PRT  
ORGANISM: Sporidiobolus salmonicolor  
US-10-989-488A-35

Query Match 66.8%; Score 65.5; DB 5; Length 343;  
Best Local Similarity 88.9%; Pred. No. 0.031;  
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 4 DNAVLEGSIVKVTGANG 20  
Db 5 DNAVLEGSIVLVGTGANG 22

RESULT 8  
US-10-989-488A-37  
Sequence 37, Application US/10989488A  
Publication No. US20050196774A1  
GENERAL INFORMATION:  
APPLICANT: Rozzell, J. David  
APPLICANT: Bui, Peter  
APPLICANT: Hua, Ling  
TITLE OF INVENTION: SYNTHETIC GENES FOR ENHANCED EXPRESSION  
FILE REFERENCE: B583:53896  
CURRENT APPLICATION NUMBER: US/10/989,488A  
CURRENT FILING DATE: 2004-11-15  
PRIOR APPLICATION NUMBER: 09/494,921  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 09/734,237  
PRIOR FILING DATE: 2000-12-08  
NUMBER OF SEQ ID NOS: 79  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO: 37  
LENGTH: 343  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic protein derived from Sporidiobolus salmonicolor  
OTHER INFORMATION: NADPH-Dependent Aldehyde Reductase 2, having an ala to gly  
OTHER INFORMATION: mutation at amino acid position 2  
US-10-989-488A-37

Query Match 66.8%; Score 65.5; DB 5; Length 343;  
Best Local Similarity 88.9%; Pred. No. 0.031;  
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 4 DNAVLEGSIVKVTGANG 20  
Db 5 DNAVLEGSIVLVGTGANG 22

RESULT 9  
US-10-437-963-171580  
Sequence 171580, Application US/10437963  
Publication No. US20040123343A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei

APPLICANT: Wu, Wei  
APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad  
APPLICANT: Li, Ping  
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963  
CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966  
SEQ ID NO: 171580  
LENGTH: 279  
TYPE: PRT  
ORGANISM: Oryza sativa  
FEATURE:  
OTHER INFORMATION: clone ID: PAT\_MRT4530\_6979C.1.pep  
US-10-437-963-171580

Query Match 52.0%; Score 51; DB 4; Length 279;  
Best Local Similarity 62.5%; Pred. No. 6.4;  
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 DNAVLEGSIVKVTGAN 19  
Db 71 DSPILVGSIVKVTGNG 86

RESULT 10  
US-10-282-122A-65763  
Sequence 65763, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haeselbeck, Robert  
APPLICANT: Ohlsen, Kari  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITRA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,076  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06  
PRIOR APPLICATION NUMBER: 60/230,347  
PRIOR FILING DATE: 2000-09-09  
PRIOR APPLICATION NUMBER: 60/242,578  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 60/253,625  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/257,931  
PRIOR FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: 60/267,636  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: 60/269,308  
PRIOR FILING DATE: 2001-02-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 78614  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 65763  
LENGTH: 636

TYPE: PRT  
ORGANISM: Neisseria meningitidis  
US-10-282-122A-65763

Query Match 49.0%; Score 48; DB 4; Length 636;  
Best Local Similarity 54.5%; Pred. No. 54;  
Matches 12; Conservative 1; Mismatches 5; Indels 4; Gaps 1;

QY 3 PDNAVEGSLVKVTGANG 20  
DB 268 PDNRRLMSADIEGKTVMVTGAGG 289

## RESULT 11

US-10-425-115-273937  
Sequence 273937, Application US/10425115  
Publication No. US20040214272A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.  
APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants  
FILE REFERENCE: 38-21(5322)B  
CURRENT APPLICATION NUMBER: US/10/425,115  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ. ID NOS: 369326  
SEQ. ID NO 273937  
LENGTH: 892  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(892)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: MRT4577\_181416C.1.pep  
US-10-425-115-273937

Query Match 49.0%; Score 48; DB 4; Length 892;  
Best Local Similarity 55.6%; Pred. No. 80;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 PDNAVEGSLVKVTGANG 20  
DB 202 PPNALLSASLLKVAQONG 219

## RESULT 12

US-10-425-114-58466  
Sequence 58466, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ. ID NOS: 73128  
SEQ. ID NO 58466  
LENGTH: 947  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: 700383178\_FLI.pep  
US-10-425-114-58466

Query Match 49.0%; Score 48; DB 4; Length 947;  
Best Local Similarity 55.6%; Pred. No. 86;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 PDNAVEGSLVKVTGANG 20  
DB 256 PPNALLSASLLKVAQONG 273

## RESULT 13

US-10-425-114-70492  
Sequence 70492, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jindong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E.  
APPLICANT: Tabaska, Jack E.  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(5313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ. ID NOS: 73128  
SEQ. ID NO 70492  
LENGTH: 965  
TYPE: PRT  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: UC-ZMFLB73025E08\_FLI.pep  
US-10-425-114-70492

Query Match 49.0%; Score 48; DB 4; Length 965;  
Best Local Similarity 55.6%; Pred. No. 88;  
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 PDNAVEGSLVKVTGANG 20  
DB 274 PPNALLSASLLKVAQONG 291

## RESULT 14

US-10-282-122A-67793  
Sequence 67793, Application US/10282122A  
Publication No. US20040029129A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Liangsu  
APPLICANT: Zamudio, Carlos  
APPLICANT: Malone, Cheryl  
APPLICANT: Haselbeck, Robert  
APPLICANT: Ohlsen, Karl  
APPLICANT: Zyskind, Judith  
APPLICANT: Wall, Daniel  
APPLICANT: Trawick, John  
APPLICANT: Carr, Grant  
APPLICANT: Yamamoto, Robert  
APPLICANT: Forsyth, R.  
APPLICANT: Xu, H.  
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms  
FILE REFERENCE: ELITPA.034A  
CURRENT APPLICATION NUMBER: US/10/282,122A  
CURRENT FILING DATE: 2003-02-20  
PRIOR APPLICATION NUMBER: 60/191,078  
PRIOR FILING DATE: 2000-03-21  
PRIOR APPLICATION NUMBER: 60/206,848  
PRIOR FILING DATE: 2000-05-23  
PRIOR APPLICATION NUMBER: 60/207,727  
PRIOR FILING DATE: 2000-05-26  
PRIOR APPLICATION NUMBER: 60/230,335  
PRIOR FILING DATE: 2000-09-06

Search completed: March 11, 2006, 05:16:11  
Job time : 93.6984 secs

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PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patent version 3.1
SEQ ID NO 67793
LENGTH: 6310
TYPE: PRT
ORGANISM: Pseudomonas putida
US-10-282-122A-67793

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Query Match 48.0%; Score 47; DB 4; Length 6310;
Best Local Similarity 37.5%; Pred. No. 1.2e+03;
Matches 12; Conservative 2; Mismatches 6; Indels 12; Gaps 1;

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Qy 1 AIPDNVAVL-----EGSLVKVTGANG 20
Db 4440 ATPDNLILAADGLSVSGTAAGSTIKVYGPNG 4471

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RESULT 15
US-10-450-763-58735
Sequence 58735, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hybeq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 58735
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (92)..(104)
OTHER INFORMATION: GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE domain
OTHER INFORMATION: Identified by eMATRIX, accession number PR00081B, p-value=6.727e-
OTHER INFORMATION: 11, raw score of 10.38
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (15)..(131)
OTHER INFORMATION: short chain dehydrogenase domain identified by Pfam,
OTHER INFORMATION: accession name adh_short, E-value=9.1e-05, Pfam score of -12.5
US-10-450-763-58735

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Query Match 46.9%; Score 46; DB 5; Length 133;
Best Local Similarity 52.6%; Pred. No. 18;
Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

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Qy 1 AIPDNVAVLEGLVKVTGAN 19
Db 5 ACPSKATIPGKTVIYVIGAN 23

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Db 1 MAQVENEV--KGKLVLTGASG 20

RESULT 4  
Q6MYZ7 ASPFU PRELIMINARY; PRT; 352 AA.

AC Q6MYZ7;  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Oxidoreductase, putative (EC 1.-.-.-).  
GN ORFNames=AfA24A6.070C;  
OS Aspergillus fumigatus (Sartorya fumigata).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
NCBI\_TaxID=5085;  
RN NUCLEOTIDE SEQUENCE.  
RP PubMed=1498527; DOI=10.1016/j.fgb.2003.12.003;  
RA Pain A., Woodward J., Quail M.A., Anderson M.J., Clark R., Collins M.,  
RA Foster N., Fraser A., Harris D., Larke N., Murphy L., Humphrey S.,  
RA O'Neill S., Petrea M., Price C., Rabinowitsch E., Rajandream M.A.,  
RA Salzberg S., Saunders D., Seegar S., Sharp S., Warren T.,  
RA Denning D.W., Barrett B., Hall N.;  
RT "Insight into the genome of Aspergillus fumigatus: analysis of a 922  
kb region encompassing the nitrate assimilation gene cluster."  
RL Fungal Genet. Biol. 41:443-453(2004).  
DR EMBL; BX649605; CAB47862.1; -; Genomic DNA.  
DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
DR InterPro; IPR001509; Epimerase\_Dh.  
DR Pfam; PF03370; Epimerase; 1.  
KW Oxidoreductase.  
SQ SEQUENCE 352 AA; 39420 MW; 0E84223EEC87ABF9 CRC64;

Query Match 54.2%; Score 58; DB 2; Length 352;  
Best Local Similarity 50.0%; Pred. No. 5;  
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MAKINAVPBGSLVLTGANG 22  
DB 1 MGS LAPTVPGGLVLTGVNG 22

RESULT 5  
Q4MSW9 ASPFU PRELIMINARY; PRT; 352 AA.  
AC Q4MSW9;  
DT 13-SEP-2005 (TREMBLrel. 31, Created)  
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)  
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)  
DE Aldenhyde reductase 11.  
GN ORFNames=Atu11360;  
OS Aspergillus fumigatus Af293.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eutotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
NCBI\_TaxID=330879;  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=Af293;  
RA Nierman W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley.,  
RA Ariyos J., Bertman M., Abe K., Archer D.B., Bermejo C., Bennett J.,  
RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,  
RA Farman M., Fedorova N., Fedorova N., Feldblum T.V., Fischer R.,  
RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,  
RA Goldman G.H., Goni K., Griffith-Jones S., Gwilliam R., Haas B.,  
RA Haas H., Harris D., Horlitch H., Huang J., Humphrey S., Jimenez J.,  
RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulcarani R.,  
RA Kumagai T., Lafont A., Latge J.-P., Li W., Lord A., Lu C.,  
RA Majoros W.H., May G.S., Miller B.L., Mahmoud Y., Molina M., Monod M.,  
RA Moutyva I., Mulligan S., Murphy L., O'Neill S., Paulsen I.,  
RA Penava M.A., Petrea M., Price C., Pritchard B.L., Quail M.A.,  
RA Rabinowitsch E., Rawlins N., Rajandream M.A., Reichard U.,

RA Renaud H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,  
RA Roming C.M., Rutter S., Salzberg S.L., Sanchez M.,  
RA Sanchez-Petereiro J.C., Saunders D., Seeger K., Squares R., Squares S.,  
RA Takeuchi M., Tekala F., Turner G., Vazquez de Aldana C.R., Weidman J.,  
RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Arai K.,  
RA Machida M., Hall N., Barrett B., Denning D.W.;  
RT "Genomic sequence of the pathogenic and allergenic filamentous fungus  
Aspergillus fumigatus.";  
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AAF0100004; FAL90463.1; -; Genomic DNA.  
SQ SEQUENCE 352 AA; 39420 MW; 0E84223EEC87ABF9 CRC64;

Query Match 54.2%; Score 58; DB 2; Length 352;  
Best Local Similarity 50.0%; Pred. No. 5;  
Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MAKINAVPBGSLVLTGANG 22  
DB 1 MGS LAPTVPGGLVLTGVNG 22

RESULT 6  
Q5ASZ7 EMENI PRELIMINARY; PRT; 341 AA.  
AC Q5ASZ7;  
DT 10-MAY-2005 (TREMBLrel. 30, Created)  
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)  
DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)  
DE Hypothetical protein.  
GN ORFNames=AN8583.2;  
OS Aspergillus nidulans FGSC A4.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eutotiales; Trichocomaceae; Emericella.  
NCBI\_TaxID=227321;  
RN NUCLEOTIDE SEQUENCE.  
RP STRAIN=FGSC A4;  
RA Birren B., Nuebaum C., Abouelleil A., Allen N., Anderson S.,  
RA Arachchi H.M., Barina N., Bastien V., Bloom T., Boguslavsky L.,  
RA Boukhalter B., Butler J., Calvo S.E., Camarata J., Chang J.,  
RA Diaz J.S., Dodge S., Dooley K., Cooke P., Corum B., DeArillano K.,  
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,  
RA Gardina S., Gierke S., Graham L., Grand-Pierre N., Haez N.,  
RA Hagopian D., Hages B., Hall J., Horton L., Hulme W., Iliev I.,  
RA Jaffe D., Johnson R., Jones C., Kamel M., Kamat A., Karatas A.,  
RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,  
RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,  
RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menes L.,  
RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,  
RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,  
RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,  
RA Rachupka A., Ramsamy U., Raymond C., Retta R., Rise C., Rogov P.,  
RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Shatrov S.,  
RA Smith C., Spencer S., Stange-Thomann N., Stojanovic N., Stubbs M.,  
RA Talmas J., Testaye S., Theodore J., Topham K., Travers M.,  
RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,  
RA Wu X., Wyman D., Young G., Zainoun J., Zambok L., Zimmer A., Zody M.,

RA Lander B.;  
RT "Genome Sequence of Aspergillus nidulans.";  
RT Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.  
CC -! CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
DR EMBL; AACD0100158; EAA60617.1; -; Genomic DNA.  
SQ SEQUENCE 341 AA; 37852 MW; 9381BB9083B3F9EA CRC64;

Query Match 51.4%; Score 55; DB 2; Length 341;  
Best Local Similarity 66.7%; Pred. No. 13;





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RL Science 286:1571-1577(1999).
DR EMBL: AE002069; AAF1927.1; -, Genomic_DNA.
DR PIR: F75279; F75279.
DR TIGR: DR2381; -.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR GO: GO:0008152; P:metabolism; IEA.
DR InterPro: IPR02086; Aldenhyd_dehydrog.
DR InterPro: IPR02539; Maoc dehydratae.
DR InterPro: IPR011966; Paan-DH.
DR Pfam: PF00171; Aldedh; 1.
DR Pfam: PF01575; Maoc_dehydratae; 1.
DR TIGRFAMs: TIGR02278; Paan-DH; 1.
DR Complete proteome.
SQ SEQUENCE 700 AA; 75493 MW; E3F6FDA72C9E932 CRC64;

Query Match 51.4%; Score 55; DB 2; Length 700;
Best Local Similarity 63.2%; Pred. No. 28;
Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 4 IDNALPEGSILVLTGANG 22
Db 203 IASGILPEGSILQVLTGDPG 221

RESULT 11
O6WE58_PINMO PRELIMINARY; PRT; 206 AA.
ID O6WE58_PINMO PRELIMINARY;
AC O6WE58_PINMO PRELIMINARY;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative NBS-LRR protein C618 (Fragment).
GN Name=RGA;
OS Pinus monticola (Western white pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
OX NCBI_TaxId=3345;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14586641; DOI=10.1007/s00438-003-0940-1;
RA Liu J.-J., Ekramoddoullah A.K.M.;
RT "Isolation, genetic variation and expression of TIR-NBS-LRR resistance
RT gene analogs from western white pine (Pinus monticola Dougl. ex. D.
RT Don.).";
RL Mol. Genet. Genomics 270:432-441(2004).
DR EMBL: AY294116; AAQ57161.1; -, mRNA.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00931; NB-ARC; 1.
FT NON_TER 1
FT NON_TER 206
FT SEQUENCE 206 AA; 23705 MW; 9A72894D0F7CECD9 CRC64;

Query Match 50.5%; Score 54; DB 2; Length 206;
Best Local Similarity 68.8%; Pred. No. 11;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 6 NAVLPEGSILVLTGAN 21
Db 20 NDVLPESGSLVLTSRN 35

RESULT 12
O6WE60_PINMO PRELIMINARY; PRT; 206 AA.
ID O6WE60_PINMO PRELIMINARY;
AC O6WE60_PINMO PRELIMINARY;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative NBS-LRR protein C605 (Fragment).
GN Name=RGA;
OS Pinus monticola (Western white pine).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
OX NCBI_TaxId=3345;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14586641; DOI=10.1007/s00438-003-0940-1;
RA Liu J.-J., Ekramoddoullah A.K.M.;
RT "Isolation, genetic variation and expression of TIR-NBS-LRR resistance
RT gene analogs from western white pine (Pinus monticola Dougl. ex. D.
RT Don.).";
RL Mol. Genet. Genomics 270:432-441(2004).
DR EMBL: AY294107; AAQ57159.1; -, mRNA.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00931; NB-ARC; 1.
FT NON_TER 1
FT NON_TER 206
FT SEQUENCE 206 AA; 23720 MW; C2D2A34E5A1FBAEC CRC64;

Query Match 50.5%; Score 54; DB 2; Length 206;
Best Local Similarity 68.8%; Pred. No. 11;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 6 NAVLPEGSILVLTGAN 21
Db 20 NDVLPESGSLVLTSRN 35

RESULT 13
O6WE61_PINMO PRELIMINARY; PRT; 206 AA.
ID O6WE61_PINMO PRELIMINARY;
AC O6WE61_PINMO PRELIMINARY;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Putative NBS-LRR protein C603 (Fragment).
GN Name=RGA;
OS Pinus monticola (Western white pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
OX NCBI_TaxId=3345;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14586641; DOI=10.1007/s00438-003-0940-1;
RA Liu J.-J., Ekramoddoullah A.K.M.;
RT "Isolation, genetic variation and expression of TIR-NBS-LRR resistance
RT gene analogs from western white pine (Pinus monticola Dougl. ex. D.
RT Don.).";
RL Mol. Genet. Genomics 270:432-441(2004).
DR EMBL: AY294106; AAQ57158.1; -, mRNA.
DR GO: GO:0005524; P:ATP binding; IEA.
DR GO: GO:0006915; P:apoptosis; IEA.
DR InterPro: IPR002182; NB-ARC.
DR Pfam: PF00931; NB-ARC; 1.
FT NON_TER 1
FT NON_TER 206
FT SEQUENCE 206 AA; 23750 MW; DEC6F629247DB19F8 CRC64;

Query Match 50.5%; Score 54; DB 2; Length 206;
Best Local Similarity 68.8%; Pred. No. 11;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 6 NAVLPEGSILVLTGAN 21
Db 20 NDVLPESGSLVLTSRN 35

RESULT 14
O6WE65_PINMO PRELIMINARY; PRT; 206 AA.
ID O6WE65_PINMO PRELIMINARY;
AC O6WE65_PINMO PRELIMINARY;
DT 05-JUL-2004 (TREMBlrel. 27, Created)

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Search completed: March 11, 2006, 05:08:43  
 Job time : 132.905 secs

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DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Putative NBS-LRR protein GM01 (Fragment).
GN Name=RGA;
OS Pinus monticola (Western white pine);
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Strobus.
OX NCBI_TaxID=3345;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=14586641; DOI=10.1007/s00438-003-0940-1;
RA Liu J.-J., Ekramoddoullah A.K.M.;
RT "Isolation, genetic variation and expression of TIR-NBS-LRR resistance
RT gene analogs from Western white pine (Pinus monticola Dougl. ex. D.
RT Don.)";
RL Mol. Genet. Genomics 270:432-441(2004).
DR EMBL; AY294096; AA057154.1; -; Genomic_DNA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR InterPro; IPR002182; NB-ARC.
DR Pfam; PF00931; NB-ARC; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 206 AA; 23808 MW; 73A5FFCDB9F5C0D7 CRC64;

Query Match 50.5%; Score 54; DB 2; Length 206;
Best Local Similarity 68.8%; Pred. No. 11;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 NAVLPEGSLLVLTGAN 21
Db 20 NDVLPSCSLIVTSRN 35

RESULT 15
Q6HC40_BACHK PRELIMINARY; PRT; 250 AA.
ID Q6HC40;
AC Q6HC40;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Glucanase permealase, C-terminal, Gntp family.
DE Name=gntP; OrderedLocuNames=BT9727_4574;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxID=180856;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=97-27;
RA Bretlin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Rice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017355; AA060986.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0015128; F:glucanase transporter activity; IEA.
DR GO; GO:0015725; F:glucanase transport; IEA.
DR InterPro; IPR003474; G1cn_transporter.
DR Pfam; PF02447; GntP_permealase; 1.
KM Complete proteome.
SQ SEQUENCE 250 AA; 26921 MW; 3BC16A20C586C23C CRC64;

Query Match 50.5%; Score 54; DB 2; Length 250;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 5 DNAVLPESGLVLTGAN 22
Db 104 DESLLPWGSLITIGAG 121

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C/Accession: A83785  
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaaki, R.; Masui, N.; Fuji, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A/Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and  
 A/Reference number: A83650; MUID:20512582; PMID:11058132  
 A/Accession: A83785  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-274 <STO>  
 A/Cross-references: UNIPROT:Q9KDY0; UNIPARC:UPI00000C3AAF; GB:AP001510; GB:BA000004; NIT  
 A/Experimental source: strain C-125  
 C/Genetics:  
 A/Gene: fhvC  
 C/Superfamily: inner membrane protein malK; ATP-binding cassette homology

Query Match 46.7%; Score 50; DB 2; Length 274;  
 Best Local Similarity 47.1%; Pred. No. 6.4;  
 Matches 8; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

OY 6 NAVLEPESGLVLTGANG 22  
 |||||:|||||  
 Db 23 NIAPEGKTIITIGANG 39

RESULT 9  
 A10445  
 probable zinc-binding dehydrogenase [imported] - *Yersinia pestis* (strain CO92)  
 C/Species: *Yersinia pestis*  
 C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 A/Accession: A10445  
 R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tlhalil, R.W.; Holden, M.T.G.; Prentice, M.B.  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,  
 Nature 413, 523-527, 2001  
 A/Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
 A/Reference number: AB0001; MUID:21470413; PMID:11586360  
 A/Accession: A10445  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-325 <KIB>  
 A/Cross-references: UNIPROT:O8ZAM8; UNIPARC:UPI00000DCTDA; GB:AL590842; PIDN:CNQ93133.1;  
 C/Genetics:  
 A/Gene: YPO3663  
 C/Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 45.8%; Score 49; DB 2; Length 325;  
 Best Local Similarity 50.0%; Pred. No. 11;  
 Matches 11; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MAKINAVLEPESGLVLTGANG 22  
 |||||:|||||  
 Db 136 MALEBGGVTPKSGEVVITGASG 157

RESULT 9  
 G71154  
 probable adenylosuccinate synthetase - *Pyrococcus horikoshii*  
 C/Species: *Pyrococcus horikoshii*  
 C/Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 09-Jul-2004  
 A/Accession: G71154  
 R/Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin  
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi  
 DNA Res. 5, 55-76, 1998  
 A/Title: Complete sequence and gene organization of the genome of a hyper-thermophilic  
 A/Reference number: A71000; MUID:98344137; PMID:9679194  
 A/Accession: G71154  
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A/Molecule type: DNA  
 A/Residues: 1-339 <KAW>  
 A/Cross-references: UNIPROT:O58187; UNIPARC:UPI000012B05; GB:AP000002; NID:G3236129; PI  
 A/Experimental source: strain OT3  
 A/Note: this accession replaces an interim accession for a sequence replaced by GenBank  
 C/Genetics:

A/Gene: PHO438

Query Match 45.8%; Score 49; DB 2; Length 339;  
 Best Local Similarity 64.7%; Pred. No. 11;  
 Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

OY 6 NAVLEPESGLVLTGANG 22  
 |||||:|||||  
 Db 164 NDALDEGSLVLTGANG 180

RESULT 10  
 E75385  
 carboxylate kinase, pfkB family - *Deinococcus radiodurans* (strain R1)  
 C/Species: *Deinococcus radiodurans*  
 C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
 A/Accession: E75385  
 R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; H  
 S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Ullrich, T.; Zalewski, C.; Ma  
 Science 286, 1571-1577, 1999  
 A/Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.  
 A/Reference number: A75250; MUID:20036896; PMID:10567266  
 A/Accession: E75385  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-311 <WHI>  
 A/Cross-references: UNIPROT:Q9RU69; UNIPARC:UPI00000DSE78; GB:AE001996; GB:AE000513; NID  
 A/Experimental source: strain R1  
 C/Genetics:  
 A/Gene: DR1525  
 A/Map position: 1  
 C/Superfamily: ribokinase

Query Match 44.9%; Score 48; DB 2; Length 311;  
 Best Local Similarity 66.7%; Pred. No. 15;  
 Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 NAVLEPESGLVLTGANG 20  
 |||||:|||||  
 Db 242 DAVLEPESGLVLTGANG 256

RESULT 11  
 B90054  
 gluconate permease [imported] - *Staphylococcus aureus* (strain N315)  
 C/Species: *Staphylococcus aureus*  
 C/Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
 A/Accession: B90054  
 R/Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc  
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;  
 C.; Shiba, T.; Hattori, M.; Ogatawara, N.; Hayashi, H.; Hiratake, K.  
 Lancet 357, 1225-1240, 2001  
 A/Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.  
 A/Reference number: A89758; MUID:21311952; PMID:11418146  
 A/Accession: B90054  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-452 <KUR>  
 A/Cross-references: UNIPROT:Q9RUD0; UNIPARC:UPI000005488A; GB:BA000018; PID:G13702455; P  
 C/Genetics:  
 A/Gene: gntP  
 C/Superfamily: D-serine permease

Query Match 44.9%; Score 48; DB 2; Length 452;  
 Best Local Similarity 36.4%; Pred. No. 22;  
 Matches 8; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 1 MAKINAVLEPESGLVLTGANG 22  
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 Db 303 MESVNAIYPIOMMLITIGCGG 324



```
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thebydy
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 32256
LENGTH: 388
TYPE: PRT
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(388)
OTHER INFORMATION: Ceres Seq. ID no. 13592517
US-11-096-568A-32256

Query Match      43.4%; Score 42.5; DB 7; Length 388;
Best Local Similarity 28.9%; Pred. No. 26;
Matches 11; Conservative 4; Mismatches 2; Indels 21; Gaps 1;

Qy      3 PDNAVLEGSIV-----KVTGAN 19
Db      160 PDVCVDSGLITATYEGHPERITQLFVXALGSKITGAN 197

RESULT 8
US-11-096-568A-20894
Sequence 20894, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thebydy
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20894
LENGTH: 210
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(210)
OTHER INFORMATION: Ceres Seq. ID no. 12390165
US-11-096-568A-20894

Query Match      42.9%; Score 42; DB 7; Length 210;
Best Local Similarity 57.1%; Pred. No. 15;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AIPDNVLEGSIVK 14
Db      108 ALPDTSVLRGTLOK 121

RESULT 9
US-11-096-568A-20893
Sequence 20893, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thebydy
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 20893
LENGTH: 277
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TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(277)
OTHER INFORMATION: Ceres Seq. ID no. 12390164
US-11-096-568A-20893

Query Match      42.9%; Score 42; DB 7; Length 277;
Best Local Similarity 57.1%; Pred. No. 21;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AIPDNVLEGSIVK 14
Db      175 ALPDTSVLRGTLOK 188

RESULT 10
US-11-096-568A-1267
Sequence 1267, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thebydy
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1267
LENGTH: 246
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(246)
OTHER INFORMATION: Ceres Seq. ID no. 13624403
US-11-096-568A-1267

Query Match      42.3%; Score 41.5; DB 7; Length 246;
Best Local Similarity 57.9%; Pred. No. 22;
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

Qy      3 PDNAVLEGSIVKVTGAN 20
Db      221 PRAVAVLQSQSOKALGANG 239

RESULT 11
US-11-096-568A-1266
Sequence 1266, Application US/11096568A
Publication No. US20060048240A1
GENERAL INFORMATION:
APPLICANT: Alexandrov, Nikolai et al.
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thebydy
FILE REFERENCE: 2750-1592PUS2
CURRENT APPLICATION NUMBER: US/11/096,568A
CURRENT FILING DATE: 2005-04-01
NUMBER OF SEQ ID NOS: 34471
SEQ ID NO 1266
LENGTH: 283
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(283)
OTHER INFORMATION: Ceres Seq. ID no. 13624402
US-11-096-568A-1266

Query Match      42.3%; Score 41.5; DB 7; Length 283;
Best Local Similarity 57.9%; Pred. No. 26;
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;
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QY 3 PDNAV-LEGSIVKVTGANG 20  
Db 258 PKRAVLQGSQEKALGANG 276

## RESULT 12

US-11-096-568A-1265  
; Sequence 1265, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Thierby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 1265  
; LENGTH: 316  
; TYPE: PRT  
; ORGANISM: Zea mays subsp. mays  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(316)  
; OTHER INFORMATION: Ceres Seq. ID no. 13624401  
US-11-096-568A-1265

Query Match 42.3%; Score 41.5; DB 7; Length 316;  
Best Local Similarity 57.9%; Pred. No. 30;  
Matches 11; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

QY 3 PDNAV-LEGSIVKVTGANG 20  
Db 291 PKRAVLQGSQEKALGANG 309

## RESULT 13

US-11-052-554A-211  
; Sequence 211, Application US/11052554A  
; Publication No. US20050288866A1  
; GENERAL INFORMATION:  
; APPLICANT: Sachdeva, et al.  
; TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE  
; TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL  
; FILE REFERENCE: 30853/40359A  
; CURRENT APPLICATION NUMBER: US/11/052,554A  
; CURRENT FILING DATE: 2005-02-07  
; PRIOR APPLICATION NUMBER: US 60/589,227  
; PRIOR FILING DATE: 2004-07-20  
; PRIOR APPLICATION NUMBER: IN 173/DEL/2004  
; PRIOR FILING DATE: 2004-02-06  
; NUMBER OF SEQ ID NOS: 763  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 211  
; LENGTH: 1562  
; TYPE: PRT  
; ORGANISM: Streptococcus mutans UA159  
US-11-052-554A-211

Query Match 42.3%; Score 41.5; DB 7; Length 1562;  
Best Local Similarity 52.6%; Pred. No. 2,1e+02;  
Matches 10; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 3 PDNAV-LEGSIVKVTGANG 20  
Db 1210 PEBALRLQDLVKITDANG 1228

RESULT 14  
US-11-096-568A-12932  
; Sequence 12932, Application US/11096568A  
; Publication No. US20060048240A1

; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; TITLE OF INVENTION: Thierby  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01  
; NUMBER OF SEQ ID NOS: 34471  
; SEQ ID NO 12932  
; LENGTH: 234  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(234)  
; OTHER INFORMATION: Ceres Seq. ID no. 14313384  
US-11-096-568A-12932

Query Match 41.8%; Score 41; DB 7; Length 234;  
Best Local Similarity 50.0%; Pred. No. 25;  
Matches 8; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 PDNAVLEGSIVKVTGA 18  
Db 71 PDGFCIESNVVKVIGA 86

RESULT 15  
US-11-098-686-10580  
; Sequence 10580, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10580  
; LENGTH: 235  
; TYPE: PRT  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-10580

Query Match 41.8%; Score 41; DB 7; Length 235;  
Best Local Similarity 58.3%; Pred. No. 25;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 EGSLVKVTGANG 20  
Db 27 EGRIVSIIGANG 38

Search completed: March 11, 2006, 05:16:52  
Job time: 11.7937 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: March 11, 2006, 05:02:47 ; Search time 18.4127 Seconds  
(without alignments)  
104.511 Million cell updates/sec

Title: US-10-616-320A-1

Perfect score: 98  
Sequence: 1 AIPDNAVLEGS LVKVTGANG 20

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	51	52.0	277	2	AF2947	hypothetical prote
2	51	52.0	277	2	D98335	ABC transporter, A
3	49	50.0	592	2	B83231	probable short-cha
4	48	49.0	636	2	G81983	pilin glycosylatio
5	48	49.0	778	2	AF2697	two component sens
6	48	49.0	778	2	AF2697	non-motile and pha
7	47	48.0	111	2	D85608	hypothetical prote
8	47	48.0	181	2	D90218	15U ribosomal prot
9	46	46.9	371	2	H70326	hypothetical prote
10	46	46.9	532	2	T06029	hypothetical prote
11	46	46.9	1647	2	T32934	hypothetical prote
12	45.5	46.4	653	2	A32687	lysyl endopeptidase
13	45	45.9	408	2	T33939	probable alcohol d
14	45	45.9	536	2	B46230	RNA-binding protei
15	45	45.9	615	2	S24761	Cpo 61.1 protein -
16	45	45.9	616	2	A46230	RNA-binding protei
17	45	45.9	930	2	T08588	hypothetical prote
18	44	44.9	327	4	S29876	probable H+-transp
19	44	44.9	501	2	S17916	H+-transporting tw
20	44	44.9	491	2	A69415	conserved hypothet
21	44	44.9	506	2	S33922	H+-transporting tw
22	44	44.9	506	2	S46508	H+-transporting tw
23	44	44.9	507	1	PWRPA	H+-transporting tw
24	44	44.9	507	1	S12309	H+-transporting tw
25	44	44.9	508	1	PMZWM	H+-transporting tw
26	44	44.9	508	2	S29792	H+-transporting tw
27	44	44.9	508	2	S26979	H+-transporting tw
28	44	44.9	509	1	PMNTAC	H+-transporting tw
29	44	44.9	509	1	PMRZAM	H+-transporting tw

30	44	44.9	509	1	PMWTAM	H+-transporting tw
31	44	44.9	510	2	S19261	H+-transporting tw
32	44	44.9	510	2	S10997	H+-transporting tw
33	44	44.9	511	2	S07316	H+-transporting tw
34	43	43.9	87	1	F71194	probable ribosomal
35	43	43.9	206	2	F69490	conserved hypothet
36	43	43.9	232	2	G84382	cobalt transport A
37	43	43.9	240	2	AB2750	hypothetical prote
38	43	43.9	240	2	A97531	branched-chain ami
39	43	43.9	252	2	AH3618	high-affinity bran
40	43	43.9	283	2	S41412	tetrahydroxynaphth
41	43	43.9	346	2	C81654	tryptophanyl-tRNA
42	43	43.9	362	1	LPECRA	rare lipoprotein A
43	43	43.9	362	2	C85563	a minor lipoprotei
44	43	43.9	362	2	G90712	modulation competi
45	43	43.9	425	2	H70456	

ALIGNMENTS

RESULT 1  
AF2947  
hypothetical protein Atu180 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)  
C:Species: Agrobacterium tumefaciens  
C:Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 09-Jul-2004  
C:Accession: AF2947  
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell  
: Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; MUID:21608550; PMID:11743193  
A:Accession: AF2947  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-277 <KUR>  
A:Cross-references: UNIPROT:Q8UB37, UNIPARC:UPI00000D20E7, GB:AE006869, PIDN:AAI43996.1;  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu180  
A:Map position: linear chromosome  
Query Match  
Best Local Similarity 52.0%; Score 51; DB 2; Length 277;  
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;  
Qy 4 DNAVLEGS LVKVTGANG 20  
Db 25 DGAIVGSLVAVVGANG 41  
RESULT 2  
D98335  
ABC transporter, ATP-binding protein rmb0588 [imported] - Agrobacterium tumefaciens (str  
C:Species: Agrobacterium tumefaciens  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 09-Jul-2004  
C:Accession: D98335  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,  
A.; Liu, F.; Woliam, C.; Allinger, M.; Doughy, D.; Scott, C.; Jappes, C.; Markelz, B.;  
Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
A:Reference number: A97359; MUID:21608551; PMID:11743194  
A:Accession: D98335  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-277 <KUR>  
A:Cross-references: UNIPROT:Q8UB37, UNIPARC:UPI00000D20E7, GB:AE007870; PIDN:AAK90206.1;  
C:Genetics:  
A:Gene: AGR\_L\_3258  
A:Map position: linear chromosome

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Query Match      52.0%; Score 51; DB 2; Length 277;
Best Local Similarity 58.8%; Pred. No. 1.5;
Matches 10; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Cy 4 DNAAVLEGSLLVKTGANG 20
    ||| ||| ||| |||
Db 25 DGAIRAGSLTRVVGANG 41

RESULT 3
B83231
Probable short-chain dehydrogenase PA3324 [imported] - Pseudomonas aeruginosa (strain PA
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: B83231
R/Seover, C.K.; Pham, X.Q.; Ervin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,
; Loay, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: B83231
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-592 <STO>
A/Cross-references: UNIPROT:Q9HYS1, UNIPARC:UPI000000C59B4, GB:AE004754, GB:AE004091, NIT
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA3324

Query Match      50.0%; Score 49; DB 2; Length 592;
Best Local Similarity 55.6%; Pred. No. 7.1;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Cy 3 PDNAVLEGSLLVKTGANG 20
    ||| ||| ||| |||
Db 318 PDASSMNGKLVVTGAGG 335

RESULT 4
G81983
pilin glycosylation protein NMA0637 [imported] - Neisseria meningitidis (strain Z2491 se
C/Species: Neisseria meningitidis
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C/Accession: G81983
R/Parikh, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jasele, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: G81983
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-636 <PAR>
A/Cross-references: UNIPROT:Q9UTX3, UNIPARC:UPI000000C4A02, GB:AL162753, GB:AL157959, NIT
A/Experimental source: serogroup A, strain Z2491
C/Genetics:
A/Gene: pgid, NMA0637
C/Superfamily: treg protein

Query Match      49.0%; Score 48; DB 2; Length 636;
Best Local Similarity 54.5%; Pred. No. 11;
Matches 12; Conservative 1; Mismatches 5; Indels 4; Gaps 1;

Cy 3 PDN----AVLEGSLLVKTGANG 20
    ||| ||| ||| |||
Db 268 PDNRLMSADLGKTVMTGAGG 289

RESULT 5
AF2697
two component sensor kinase plec [imported] - Agrobacterium tumefaciens (strain C58, Dup
```

```
C/Species: Agrobacterium tumefaciens
C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C/Accession: AF2697
R/Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E
ter, E.W.
A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A/Reference number: AB2577; MUID:21608550; PMID:11743193
A/Accession: AF2697
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-778 <KIR>
A/Cross-references: UNIPROT:Q8UGQ3, UNIPARC:UPI000000D19D6, GB:AE008688, PIDN:AAL41996.1;
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: plec
A/Map position: circular chromosome

Query Match      49.0%; Score 48; DB 2; Length 778;
Best Local Similarity 35.0%; Pred. No. 14;
Matches 7; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Cy 1 AIPDNVLEGSLLVKTGANG 20
    ||| ||| ||| |||
Db 121 ALPSGSLADGTWLLSGSNG 140

RESULT 6
P97479
non-motile and phage-resistance protein [imported] - Agrobacterium tumefaciens (strain C
C/Species: Agrobacterium tumefaciens
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: P97479
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tume
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: P97479
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-778 <KIR>
A/Cross-references: UNIPROT:Q8UGQ3, UNIPARC:UPI000000D19D6, GB:AE007869, PIDN:AAK6791.1;
C/Genetics:
A/Gene: AGR_C_1799
A/Map position: circular chromosome

Query Match      49.0%; Score 48; DB 2; Length 778;
Best Local Similarity 35.0%; Pred. No. 14;
Matches 7; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Cy 1 AIPDNVLEGSLLVKTGANG 20
    ||| ||| ||| |||
Db 121 ALPSGSLADGTWLLSGSNG 140

RESULT 7
D85608
hypothetical protein Z1183 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: D85608; E85659
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: D85608
A/Status: preliminary
A/Molecule type: DNA
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A:Residues: 1-111 <STO>  
 A:Cross-references: UNIPROT:Q8X9P2; UNIPARC:UPI00000D07CC; GB:AE005174; NID:G12513991; F  
 A:Experimental source: strain O157:H7, substrain EDL933  
 A:Accession: E85659  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-111 <ST2>  
 A:Cross-references: UNIPARC:UPI00000D07CC; GB:AE005174; NID:G12514511; PIDN:AA655737.1;  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z1183; Z1622

Query Match 48.0%; Score 47; DB 2; Length 111;  
 Best Local Similarity 41.2%; Pred. No. 2.5;  
 Matches 7; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 PDNAVLEGSVKTGANG 19  
 DB 28 PDNAVLEGSVKTGANG 44

RESULT 8  
 D90218  
 1SU ribosomal protein L6AB (rpL6AB) [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus  
 C:Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 09-Jul-2004  
 C:Accession: D90218  
 R:Jing, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayer, M.J.; Chan-  
 arret, R.A.; Ragan, M.A.; Senese, C.W.; Van der Oost, J.  
 submitted to GenBank, April 2001  
 A:Description: Sulfolobus solfataricus complete genome.  
 A:Reference number: A99139  
 A:Accession: D90218  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-181 <KUR>  
 A:Cross-references: UNIPROT:Q9UX91; UNIPARC:UPI000013416; GB:AE006641; NID:G13813871; F  
 C:Genetics:  
 A:Gene: rpL6AB  
 C:Superfamily: ribosomal protein L6/L9

Query Match 48.0%; Score 47; DB 2; Length 181;  
 Best Local Similarity 47.6%; Pred. No. 4.2;  
 Matches 10; Conservative 4; Mismatches 5; Indels 2; Gaps 1;

QY 2 IPDNV--LEGSVKTGANG 20  
 DB 12 IPKNVVDLKGSIKIKGPKG 32

RESULT 9  
 H70326  
 hypothetical protein aq\_294 - Aquifex aeolicus

C:Species: Aquifex aeolicus  
 C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 09-Jul-2004  
 C:Accession: H70326  
 R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'  
 V.  
 Nature 392, 353-358, 1998  
 A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
 A:Reference number: A70300; MUID:98196666; PMID:9537320  
 A:Accession: H70326  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-371 <AQF>  
 A:Cross-references: UNIPROT:O66644; UNIPARC:UPI00005626F; GB:AE000682; NID:G2982979; PI  
 A:Experimental source: strain VFS  
 C:Genetics:  
 A:Gene: aq\_294

Query Match 46.9%; Score 46; DB 2; Length 371;  
 Best Local Similarity 57.1%; Pred. No. 13;

Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
 QY 2 IPDNVLEGSVKT 15  
 DB 321 IPEKALIEGNRVKI 334

RESULT 10  
 T06029  
 hypothetical protein T28119.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
 C:Accession: T06029  
 R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, G.; Ba  
 submitted to the Protein Sequence Database, March 1999  
 A:Reference number: Z15484  
 A:Accession: T06029  
 A:Molecule type: DNA  
 A:Residues: 1-532 <BEV>  
 A:Cross-references: UNIPROT:Q9T069; UNIPARC:UPI00000ABF4D; EMBL:AL035709; GSPDB:GN00062;  
 A:Experimental source: cultivar Columbia; BAC clone T28119  
 C:Genetics:  
 A:Gene: ATSP:T28119.100  
 A:Map position: 4

Query Match 46.9%; Score 46; DB 2; Length 532;  
 Best Local Similarity 52.9%; Pred. No. 20;  
 Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 PDNAVLEGSVKTGANG 19  
 DB 209 PKNEVLEGSVKEVSIN 225

RESULT 11  
 T32934  
 hypothetical protein W03D8.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans  
 C:Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
 C:Accession: T32934  
 R:Jones, K.; Graves, T.; Ozersky, P.  
 submitted to the EMBL Data Library, January 1998  
 A:Description: The sequence of C. elegans coamid W03D8.  
 A:Reference number: Z21249  
 A:Accession: T32934  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA

A:Residues: 1-1647 <JON>  
 A:Cross-references: UNIPARC:UPI0000164013; EMBL:AF043702; PIDN:AA97563.1; GSPDB:GN00019  
 A:Experimental source: strain Bristol N2; clone W03D8  
 C:Genetics:  
 A:Gene: CESP:W03D8.6  
 A:Map position: 1  
 A:Insertions: 47/1; 82/3; 115/1; 230/1; 319/2; 406/3; 466/1; 513/1; 554/2; 586/3; 653/1; 70  
 1589/2

Query Match 46.9%; Score 46; DB 2; Length 1647;  
 Best Local Similarity 83.3%; Pred. No. 66;  
 Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IPDNVLEGSV 13  
 DB 808 IGDNAVLEGSV 819

RESULT 12  
 A32687  
 lysozyme (EC 3.4.21.50) precursor - Achromobacter lyticus (strain M497-1)

N:Alternate names: Achromobacter proteinase I  
 C:Species: Achromobacter lyticus  
 C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
 C:Accession: A32687; A32960  
 R:Ohara, T.; Makino, K.; Shinagawa, H.; Nakata, A.; Norioka, S.; Sakiyama, F.

J. Biol. Chem. 264, 20625-20631, 1989  
 A;Title: Cloning, nucleotide sequence, and expression of Achromobacter protease I gene.  
 A;Reference number: A32687; PMID:90062204; PMID:2684982  
 A;Accession: A32687  
 A;Molecule type: DNA  
 A;Residues: 1-653 <ORF>  
 A;Cross-references: UNIPROT:P15636; UNIPARC:UPI0000125C8B; GB:J05128; NID:G141803; PIDN:  
 R;Tsunawawa, S.; Masaki, T.; Hirose, M.; Soejima, M.; Sakiyama, F.  
 J. Biol. Chem. 264, 3832-3839, 1989  
 A;Title: The primary structure and structural characteristics of Achromobacter lyticus F  
 A;Reference number: A32960; PMID:89139439; PMID:2492988  
 A;Accession: A32960  
 A;Molecule type: protein  
 A;Residues: 206-473 <TSU>  
 A;Cross-references: UNIPARC:UPI000011061E  
 C;Comment: This protein specifically hydrolyzes [Leu] peptide bonds including the Lys-P  
 C;Keywords: hydrolase; serine proteinase  
 F;1-20/Domain: signal sequence #status predicted <SIG>  
 F;21-205/Domain: propeptide #status predicted <PRO>  
 F;206-473/Product: achromobacter proteinase I #status experimental <MAT>  
 F;211-421.217-285.241-263/disulfide bonds: #status experimental  
 F;262,318,399/Active site: His, Asp, Ser #status predicted

Query Match 46.4%; Score 45.5; DB 2; Length 653;  
 Best Local Similarity 55.0%; Pred. No. 29;  
 Matches 11; Conservative 3; Mismatches 5; Indels 1; Gaps 1;  
 QY 1 AIPDNVLEGSIVVTGANG 20  
 Db 569 AIPDNVLEGSIVVTGANG 587

RESULT 13  
 T33939  
 Probable alcohol dehydrogenase (EC 1.1.1.1) [similarity] - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C;Accession: T33939  
 R;Becker, M.; Graves, T.; Wilson, C.  
 submitted to the EMBL Data Library, February 1999  
 A;Description: The sequence of C. elegans cosmid D2063.  
 A;Reference number: 221442  
 A;Accession: T33939  
 A;Status: preliminary; translated from GB/EMBL/DDJ  
 A;Molecule type: DNA  
 A;Residues: 1-408 <BEC>  
 A;Cross-references: UNIPROT:Q9UAT1; UNIPARC:UPI00000762B1; EMBL:AF125951; PIDN:ADD14690.  
 A;Experimental source: strain Bristol N2; clone D2063  
 C;Genetics:  
 A;Gene: CESP:D2063.1  
 A;Map position: 5  
 A;Intons: 294/3; 359/3; 373/3  
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
 C;Keywords: NAD; oxidoreductase; zinc  
 F;47,70,173/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

Query Match 45.9%; Score 45; DB 2; Length 408;  
 Best Local Similarity 45.0%; Pred. No. 21;  
 Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 AIPDNVLEGSIVVTGANG 20  
 Db 181 ALKESEVKSQIVAVTGAG 200

RESULT 14  
 B46230  
 RNA-binding protein homolog Cpo (clone 61.2) - fruit fly (Drosophila melanogaster)  
 N;Alternate names: couch potato protein 61.2; cpo61.2 protein  
 C;Species: Drosophila melanogaster  
 C;Date: 21-Sep-1993 #sequence\_revision 30-Apr-1999 #text\_change 15-Mar-2004  
 C;Accession: B46230; S24678  
 R;Belien, H.J.; Kooyer, S.; D'Evelyn, D.; Pearlman, J.

Genes Dev. 6, 2125-2136, 1992  
 A;Title: The Drosophila couch potato protein is expressed in nuclei of peripheral neurons  
 A;Reference number: A46230; PMID:93051332; PMID:1427076  
 A;Accession: B46230  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-536 <BEL>  
 A;Cross-references: UNIPARC:UPI000017BECA; GB:Z14312  
 A;Note: sequence extracted from NCBI backbone (NCBIN:117907, NCBI:P.117908)  
 R;Belien, H.J.  
 submitted to the EMBL Data Library, August 1992  
 A;Reference number: S24678  
 A;Accession: S24678  
 A;Molecule type: DNA  
 A;Residues: 1-177, 'T', 179-311, 'T', 313-319, 'G', 321-536 <BBF>  
 A;Cross-references: UNIPARC:UPI000017BECB; EMBL:Z14312  
 C;Genetics:  
 A;Gene: FlyBase:cpo  
 A;Start codon: CTC  
 C;Keywords: alternative splicing; RNA binding  
 F;453-521/Domain: ribonucleoprotein repeat homology <RRM>

Query Match 45.9%; Score 45; DB 2; Length 536;  
 Best Local Similarity 75.0%; Pred. No. 29;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 9 EGSLVVTGANG 20  
 Db 479 EGSLVVTGANG 490

RESULT 15  
 S24761  
 Cpo 61.1 protein - fruit fly (Drosophila melanogaster)  
 C;Species: Drosophila melanogaster  
 C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 15-Mar-2004  
 C;Accession: S24761  
 R;Belien, H.J.  
 submitted to the EMBL Data Library, August 1992  
 A;Reference number: S24677  
 A;Accession: S24761  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-615 <BEL>  
 A;Cross-references: UNIPARC:UPI000017BE84; EMBL:Z14974  
 C;Genetics:  
 A;Gene: FlyBase:cpo  
 A;Cross-references: FlyBase:FBgn0000363  
 A;Start codon: CTC  
 A;Intons: 450/1; 475/1; 493/3; 514/3; 562/1  
 F;452-520/Domain: ribonucleoprotein repeat homology <RRM>

Query Match 45.9%; Score 45; DB 2; Length 615;  
 Best Local Similarity 75.0%; Pred. No. 33;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 9 EGSLVVTGANG 20  
 Db 478 EGSLVVTGANG 489

Search completed: March 11, 2006, 05:09:43  
 Job time: 20.4127 secs

Db 244 AIPESLVLEGHLEKAFGRNG 263

RESULT 4  
Q65DJI\_BACLD PRELIMINARY; PRT; 396 AA.

AC Q65DJI\_062P10;  
DT 25-OCT-2004 (TREMBlrel. 28, Created)  
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)  
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)  
DE ywdb (SAM (And some other nucleotide binding motif, PUA domain).  
GN Name=ywdb; OrderedLocustNames=BL03857, BL104060;  
OS Bacillus licheniformis (strain DSM 13 / ATCC 14580).  
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
NCBI\_TaxID=279010;  
RN NCU00101;  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15383718; DOI=10.1159/000079829;  
RA Velth B., Herzberg C., Steckel S., Feesche J., Maurer K.H.,  
RA Ehrenreich P., Baumer S., Henne A., Liesegang H., Merkl R.,  
RA Ehrenreich A., Gottschalk G.;  
RT "The complete genome sequence of Bacillus licheniformis DSM13, an  
organism with great industrial potential.";  
RL J. Mol. Microbiol. Biotechnol. 7:204-211 (2004).  
[2]  
RN NUCLEOTIDE SEQUENCE.  
RX PubMed=1561803; DOI=10.1186/gb-2004-5-10-r77;  
RA Rey M.W., Ramaiya P., Nelson B.A., Brody-Karpin S.D., Zaretsky E.J.,  
RA Tang M., Lopez de Leon A., Xiang H., Gueti V., Clausen I.G.,  
RA Olsen P.B., Rasmussen M.D., Andersen J.T., Joergensen P.L.,  
RA Larsen T.S., Sorokin A., Bolotin A., Lapidus A., Galloway N.,  
RA Ehrlich S.D., Berka R.M.;  
RT "Complete genome sequence of the industrial bacterium Bacillus  
licheniformis and comparisons with closely related Bacillus species.";  
RL Genome Biol. 5:RESEARCH077.1-RESEARCH077.12(2004).  
DR EMBL; AE017333; AAU42873.1; -; Genomic DNA.  
DR EMBL; CP000002; AAU25501.1; -; Genomic DNA.  
DR GO; GO:0003723; F:RNA binding; IEA.  
DR GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.  
DR InterPro; IPR002478; PUA.  
DR SMART; SM00359; PUA; 1.  
DR PROSITE; PS00890; PUA; 1.  
KW Complete proteome.  
SQ SEQUENCE 396 AA; 44897 MW; C1FPIACSEFFFE2AB CRC64;

Query Match 52.0%; Score 51; DB 2; Length 396;  
Best Local Similarity 47.1%; Pred. No. 32;  
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 4 DNAIEGSLVKTGANG 20  
DB 30 ENGIKESLIRITDENG 46

RESULT 5  
Q9MM39\_9SPER PRELIMINARY; PRT; 412 AA.  
AC Q9MM39;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE P1 ATPase alpha subunit (Fragment).  
GN Name=atpA;  
OS Gnetum ula.  
OC Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Gnecophyta; Gnecopsida; Gnetales; Gnecaceae; Gnetum.  
NCBI\_TaxID=3383;  
RN NCU00101;  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20226063; PubMed=10760278; DOI=10.1073/pnas.97.8.4092;

RA Howe L.M., Coat G., dePamphilis C.W.;  
RT "Phylogeny of seed plants based on all three genomic compartments:  
RT extant gymnosperms are monophyletic and Gnetales' closest relatives  
RT are conifers.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:4092-4097(2000).  
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.  
DR EMBL; AF209109; AAF6467.1; -; Genomic DNA.  
DR HSSP; P19483; 1H8E.  
DR SMR; Q9MM39; 1-399.  
DR GO; GO:0005739; C:Mitochondrion; IEA.  
DR GO; GO:0005739; C:proton-transporting ATP synthase complex, C. . .; IEA.  
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0046933; F:Hydrogen-transporting ATP synthase activity. . .; IEA.  
DR GO; GO:0046961; F:Hydrogen-transporting ATPase activity, rota. . .; IEA.  
DR GO; GO:0016787; F:Hydrolase activity; IEA.  
DR GO; GO:0016820; F:Hydrolase activity, acting on acid anhydrid. . .; IEA.  
DR GO; GO:0015986; F:ATP synthase coupled proton transport; IEA.  
DR GO; GO:0006811; P:ion transport; IEA.  
DR GO; GO:0015992; P:proton transport; IEA.  
DR InterPro; IPR005294; ATP\_synthF1\_alph.  
DR InterPro; IPR004100; ATPase\_a/b\_N.  
DR InterPro; IPR000194; ATPase\_a/bcentre.  
DR Pfam; PF00006; ATP-synt\_ab; 1.  
DR Pfam; PF02874; ATP-synt\_ab\_N; 1.  
DR TIGRFAMs; TIGR00962; atpA\_1.  
DR PROSITE; PS00152; ATPASE\_ALPHA\_BETA; 1.  
KW ATP synthetase; ATP-binding; CF(1); Hydrogen ion transport; Hydrolase;  
KW ion transport; Mitochondrion; Nucleotide-binding; Transport.  
FT NON\_TER 1  
FT 412 412  
SQ SEQUENCE 412 AA; 43993 MW; 824873B6ED21327B CRC64;

Query Match 51.0%; Score 50; DB 2; Length 412;  
Best Local Similarity 60.0%; Pred. No. 47;  
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 DNAIEGSLVKTGA 18  
DB 45 DTAIEGSLVKTGS 59

RESULT 6  
Q9T7A3\_GNEGN PRELIMINARY; PRT; 418 AA.  
AC Q9T7A3;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE ATPase alpha subunit (Fragment).  
GN Name=atp1;  
OS Gnetum gnemon (Bago).  
OC Mitochondrion.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Gnecophyta; Gnecopsida; Gnetales; Gnecaceae; Gnetum.  
NCBI\_TaxID=3382;  
RN NCU00101;  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=20052162; PubMed=10586879; DOI=10.1038/46536;  
RA Qiu Y.L., Lee J., Bernasconi-Quadroni F., Solis D.E., Solis P.S.,  
RA Zanis M., Zimmer E.A., Chen Z., Savolainen V., Chase M.W.;  
RT "The earliest angiosperms: evidence from mitochondrial, plastid and  
nuclear genomes.";  
RL Nature 402:404-407(1999).  
CC -1- SIMILARITY: Belongs to the ATPase alpha/beta chains family.  
DR EMBL; AF197617; AAF19949.1; -; Genomic DNA.  
DR HSSP; P19483; 1B79.  
DR SMR; Q9T7A3; 1-418.  
DR GO; GO:0005739; C:Mitochondrion; IEA.  
DR GO; GO:0045261; C:proton-transporting ATP synthase complex, C. . .; IEA.  
DR GO; GO:0016469; C:proton-transporting two-sector ATPase complex; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0046933; F:Hydrogen-transporting ATP synthase activity. . .; IEA.

```

DR GO: GO:0046961; F:hydrogen-transporting ATPase activity, rota. . . ; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0016820; F:hydrolase activity, acting on acid anhydrid. . . ; IEA.
DR GO: GO:0015986; P:ATP synthesis coupled proton transport; IEA.
DR GO: GO:0006811; P:ion transport; IEA.
DR GO: GO:0015992; P:proton transport; IEA.
DR InterPro: IPR005294; ATPase a/b C.
DR InterPro: IPR00793; ATPase a/b C.
DR InterPro: IPR004100; ATPase a/b N.
DR InterPro: IPR00194; ATPase a/b centre.
DR Pfam: PF00006; ATP-synt_ab_1.
DR Pfam: PF00306; ATP-synt_ab_C_1.
DR Pfam: PF02874; ATP-synt_ab_N_1.
DR TIGRFAMs: TIGR00962; atpA_1.
DR PROSITE: PS00152; ATPase ALPHA BETA_1.
DR ATP synthetase; ATP-binding; CF1; Hydrogen ion transport; Hydrolase;
KM ion transport; Mitochondrion; Nucleotide-binding; Transport.
PT NON_TER 1
PT NON_TER 1
SQ SEQUENCE 418 AA; 44753 MW; 0FE55A3B5722901 CRC64;

Query Match 51.0%; Score 50; DB 2; Length 418;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 4 DNAAVLEGSIVKVTGA 18
Db 44 DTAIEGSIYKRTGS 58

RESULT 7
0691P6 ORYSA PRELIMINARY; PRT; 451 AA.
ID 0691P6 ORYSA PRELIMINARY;
AC 0691P6;
DT 25-OCT-2004 (TrEMBLrel. 28. Created)
DT 25-OCT-2004 (TrEMBLrel. 28. Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28. Last annotation update)
DE Putative aspartic proteinase nepenthesin I.
GN Name=OSJNB0039D04.13;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OC NCBI_TaxID=39947;
RN [1]
NP NUCLEOTIDE SEQUENCE.
RA Sasaki T., Matsumoto T., Katayose Y.;
RT "Oryza sativa nippohare (GA3) genomic DNA, chromosome 7, BAC
clone:OSJNB0039D04."
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AP006753; BA032124.1; -; Genomic_DNA.
DR Gramene; O691P6; -;
DR GO: GO:004194; F:protease A activity; IEA.
DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro: IPR001461; Peptidase A1.
DR InterPro: IPR001969; Pept_Asp_AS.
DR Pfam: PF00026; Asp_1.
DR PRINTS: PR00792; PEPSIN.
DR PROSITE: PS00141; ASP_PROTEASE; UNKNOWN_1.
SQ SEQUENCE 451 AA; 46440 MW; E7F24FED78353C5E CRC64;

Query Match 51.0%; Score 50; DB 2; Length 451;
Best Local Similarity 62.5%; Pred. No. 51;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 DNAAVLEGSIVKVTGAN 19
Db 243 DSPILFSLAKVTGQN 258

RESULT 8
Q4RSV8_TETNG PRELIMINARY; PRT; 687 AA.
ID Q4RSV8_TETNG PRELIMINARY;

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AC Q4RSV8;
DT 13-SEP-2005 (TrEMBLrel. 31. Created)
DT 13-SEP-2005 (TrEMBLrel. 31. Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31. Last annotation update)
DE Chromosome 12 SCAR14999, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00029526001;
OS Tetradodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodon.
OC NCBI_TaxID=99883;
RN [1]
NP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Strange-Thomann N.,
RA Mancel E., Bouneau L., Fischer C., Ozouf-Coetz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Crenaud C., Duprat S., Brotier P., Couranceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McSwan P., Bosak S.,
RA Kellis M., Volt J.N., Guigo R., Zody M.C., Nesitov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "genome duplication in the teleost fish Tetradodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
NP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: CAHE01014999; CAG08524.1; -; Genomic_DNA.
FT NON_TER 687
FT NON_TER 687
SQ SEQUENCE 687 AA; 72523 MW; 3A4531EB8D7AB537 CRC64;

Query Match 51.0%; Score 50; DB 2; Length 687;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 8; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 AIPDNAAVLEGSIVKVTGANG 20
Db 356 SVPPNVTAGSVLPVTGGRG 375

RESULT 9
06B1S4 DEBHA PRELIMINARY; PRT; 1048 AA.
ID 06B1S4 DEBHA PRELIMINARY;
AC 06B1S4;
DT 25-OCT-2004 (TrEMBLrel. 28. Created)
DT 25-OCT-2004 (TrEMBLrel. 28. Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28. Last annotation update)
DE Similar to CA1657|IPF16022 Candida albicans IPF16022 unknown
DE function.
GN OrderedLocNames=DEHA0G086799;
OS Debaryomyces hanseni (Yeast) (Torulasporea hanseni).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomycetes.
OC NCBI_TaxID=4959;
RN [1]
NP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 36239 / CBS 767;
RC PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durieux P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla B.,
RA Goffard N., Franquet L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boismere A., Boyer J., Cattolico L., Confanioleri F., de Darvar A.,

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SQ      SEQUENCE      3172 AA;   338131 MW;   351478B6BF20CFDE CRC64;
Query Match          51.0%; Score 50; DB 2; Length 3172;
Best Local Similarity 55.6%; Pred. No. 3.6e+02;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy      1 AIPDNVLEGSLVYVTGANG 20
       |||:|||:||||||
Db      2026 AYVDNALDPAFAEKVTSNG 2045

RESULT 11
O9HYS1_PSEAE PRELIMINARY; PRT; 592 AA.
ID O9HYS1_PSEAE PRELIMINARY;
AC O9HYS1;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Probable short-chain dehydrogenase.
GN OrderedLocustNames=PA3324;
OC Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023C07;
RA Stever C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,
RA Hickey R.J., Britman F.S.L., Huffnagle W.O., Kowalik D.J., Lagrou M.,
RA Gabler R.L., Goltzy L., Tolentino E., Westbrook-Wedman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Labbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., V.,
RA Reizer J., Salier M.H. Jr., Hancock R.E.W., Lozy S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AE004754; AAC06712.1; -; Genomic_DNA.
DR PIR; B83231; B83231.
DR HSSP; Q7Z4M1; 1PR9.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008153; P:metabolism; IEA.
DR InterPro; IPRO00073; A/b_hydrolase.
DR InterPro; IPRO02198; Adh_short_C2.
DR InterPro; IPRO02347; Adh_short_C2.
DR InterPro; IPRO00639; Epox_hydrolase.
DR InterPro; IPRO03379; Ser_easts.
DR Pfam; PF00561; Abhydrolase_1; 1.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00412; EPOXHYDLASE.
DR PRINTS; PR00081; GDHRDH.
DR PROSITE; PS00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome.
SQ      SEQUENCE      592 AA;   65770 MW;   7EADDD996BD4D0157 CRC64;

Query Match          50.0%; Score 49; DB 2; Length 592;
Best Local Similarity 55.6%; Pred. No. 96;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0

Qy      3 PDNAVLEGSLVYVTGANG 20
       |||:|||:||||||
Db      318 PDASMGKLVYVTGAGG 335

RESULT 12
O4ZU05_PSESY PRELIMINARY; PRT; 732 AA.
ID O4ZU05_PSESY PRELIMINARY;
AC O4ZU05;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Outer membrane autotransporter barrel precursor.

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GN ORFNames=Pyrr_2034;
OS Pseudomonas syringae pv. syringae B728a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=205918;
RN
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RG DOE Joint Genome Institute;
RA Chain P., Larimer F., DiBartolo G., Copeland A., Lykidis A., Truong S.,
RA Nolan M., Goldsman E., Thiel J., Malfatti S., Lapidus A., Deter J.C.,
RA Land M., Richardson P.M., Kyriakides N.C., Ivanova N.;
RT "Comparison of two complete genome sequences of Pseudomonas syringae
RT pv. syringae B728a and pv. tomato DC3000."
RT Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2005).
RN
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Loper J.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B728a;
RA Fell H., Fell W.S., Lindow S.E.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: CP0000075; AAY37077.1; -; Genomic_DNA.
DR InterPro: IPR005546; Auto_transp_beta.
DR InterPro: IPR006315; Auto_transp_beta.
DR InterPro: IPR004899; Pectactin.
DR InterPro: IPR003991; Pectactin_C.
DR Pfam: PF03797; Autotransporter; 1.
DR Pfam: PF03212; Pectactin; 1.
DR PRINTS: PR01484; PRACRNPAMILY.
DR TIGRFAMs: TIGR01414; autotrans_bar1; 1.
KW Signal.
KM
FT SIGNAL
SQ SEQUENCE 732 AA; 75763 MW; 4C355FC1A478A628 CRC64;

Query Match 50.0%; Score 49; DB 2; Length 722;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 NAVLEGSIVKYTGANG 20
Db 148 NLTEGTSVTATGANG 163

RESULT 13
DNL1 PYRFU
ID DNL1 PYRFU STANDARD; PRT; 561 AA.
AC P56709;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Thermotestable DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase
DE [AIP]) (Pfu DNA ligase).
GN Name=lig; OrderedLocusNames=PF1635;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PROTEIN SEQUENCE OF N-TERMINUS.
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Mathur E.J., Marsh E.J., Schoettlin W.E.;
RT "Purified thermostable Pyrococcus furiosus DNA ligase."
RT Patent number US5700672, 23-DEC-1997.
RN
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Vcl / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome."
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

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CC -1- FUNCTION: This protein seals, during DNA replication, DNA
CC recombination and DNA repair, nicks in double-stranded DNA.
CC -1- CATALYTIC ACTIVITY: ATP + (deoxyribonucleotide) (n) +
CC (deoxyribonucleotide) (m) = AMP + diphosphate +
CC (deoxyribonucleotide) (n+m).
CC -1- BIOPHYSICOCHEMICAL PROPERTIES:
CC Temperature dependence:
CC Optimum temperature is about 70 degrees Celsius. Active from 4
CC to 100 degrees Celsius. Thermostable;
CC -1- SUBUNIT: Monomer.
CC -1- SIMILARITY: Belongs to the ATP-dependent DNA ligase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC -----
DR EMBL: AE010263; AL81759.1; -; Genomic_DNA.
DR HAMAP: MF_00407; -; 1.
DR InterPro: IPR000977; DNA_ligase.
DR InterPro: IPR012309; DNA_ligase_A_C.
DR InterPro: IPR012310; DNA_ligase_A_M.
DR InterPro: IPR012308; DNA_ligase_A_N.
DR InterPro: IPR012340; OB_NA_Dd_sub.
DR PANTHER: PTHR10459; DNA_ligase; 1.
DR Pfam: PF04679; DNA_ligase_A_C; 1.
DR Pfam: PF01068; DNA_ligase_A_M; 1.
DR Pfam: PF04675; DNA_ligase_A_N; 1.
DR TIGRFAMs: TIGR00574; dnl1; 1.
DR PROSITE: PS00697; DNA_LIGASE_A1; 1.
DR PROSITE: PS00333; DNA_LIGASE_A2; FALSE_NEG.
DR PROSITE: PS50160; DNA_LIGASE_A3; 1.
KW ATP-binding; Cell cycle; Cell division; Complete proteome;
KW Direct protein sequencing; DNA damage; DNA recombination; DNA repair;
KW DNA replication; Ligase; Nucleotide-binding;
KW ACT_SITE 249 N6-AMP-lyeine intermediate (By
FT similarity).
SQ SEQUENCE 561 AA; 63773 MW; 534158525B9D24B2 CRC64;

Query Match 49.5%; Score 48.5; DB 1; Length 561;
Best Local Similarity 52.6%; Pred. No. 1.1e+02;
Matches 10; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 2 IPDNAVLEGSIVKYTGANG 20
Db 290 IPEKATVESELVAI-GENG 307

RESULT 14
O6AHE3 LEIXX
ID O6AHE3 LEIXX PRELIMINARY; PRT; 340 AA.
AC O6AHE3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Alcohol dehydrogenase.
GN Name=adh; OrderedLocusNames=Lxx01190;
OS Lelifsonia xyli (subsp. xyli).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Micrococcineae; Microbacteriaceae; Lelifsonia.
OX NCBI_TaxID=59736;
RN
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CTCB07;
RC PubMed=13305603;
RA Monteiro-Vitorello C.B., Camargo L.E.A., Van Sluys M.A.,
RA Kitajima J.P., Truffi D., do Amaral A.M., Hasekava R.,
RA de Oliveira J.C.F., Wood D., de Oliveira M.C., Miyaki C.Y.,
RA Takita M.A., da Silva A.C.R., Furlan L.R., Carraro D.M., Camarotte G.,
RA Almeida N.F., Jr., Carter H., Coutinho L.L., El-Dorri H.A.,
RA Ferro M.I.T., Gagliardi P.R., Gagliotti E., Goldman M.H.S.,
RA Goldman G.H., Kimura E.T., Ferro E.S., Kuramae E.E., Lemos E.G.M.,

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Job time : 122.095 secs

RA Lemos M.V.F., Mauro S.M.Z., Machado M.A., Marino C.L., Menck C.F.,  
 RA Nunes L.R., Oliveira R.C., Pereira G.G., Siqueira W., de Souza A.A.,  
 RA Teal S.M., Zanca A.S., Simpson A.J.G., Brumley S.M., Setubal J.C.,  
 RT "The genome sequence of the Gram-positive sugarcane pathogen *Leifsonia*  
 RT *xyli* subsp. *xyli*.";  
 RL Mol. Plant Microbe Interact. 17:827-836(2004).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).  
 DR EMBL; AE016822; AAT88202.1; -; Genomic DNA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0008270; F:zinc ion binding; IEA.  
 DR InterPro; IPR002085; ADH\_SF\_Zn.  
 DR Pfam; PF00107; ADH\_zinc\_N; I.  
 KW Complete proteome.  
 SQ SEQUENCE 340 AA; 35189 MW; D8CD56AB6F529543 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 340;  
 Best Local Similarity 60.0%; Pred. No. 79;  
 Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 AIPDNVLEGSILVKYTGANG 20  
 Db 151 ADPDRVRAEGSSVLTGAAG 170

RESULT 15  
 ID 097A08 THEVO PRELIMINARY; PRT; 404 AA.  
 AC 097A08  
 DT 01-OCT-2001 (Tremblrel. 18, Created)  
 DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Carboxypeptidase.  
 GN OrderedLocusNames=TV0751; ORFNames=TVG0758219;  
 OS Thermoplasma volcanium.  
 OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;  
 OC Thermoplasmataceae; Thermoplasmata.  
 OX NCBI\_TaxID=50339;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
 RC STRAIN=GSS1 / DSM 4299 / JCM 9571;  
 RX MEDLINE=20570466; PubMed=11121031; DOI=10.1073/pnas.97.26.14257;  
 RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,  
 RA Kawashima T., Yamamoto K., Yamazaki M., Kanehori K., Kawamoto T.,  
 RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.,  
 RT "Archaeal adaptation to higher temperatures revealed by genomic  
 RT sequence of *Thermoplasma volcanium*."  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).  
 DR EMBL; BA000011; BAB59893.1; -; Genomic\_DNA.  
 DR MEROPS; M20.008; -.  
 DR GO; GO:0004180; F:carboxypeptidase activity; IEA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
 DR GO; GO:0046983; F:protein dimerization activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR011650; M20\_dimer.  
 DR InterPro; IPR002933; Peptidase\_M20.  
 DR InterPro; IPR010168; Pept\_M20D\_amidh.  
 DR Pfam; PF01567; M20\_dimer; 1.  
 DR Pfam; PF01546; Peptidase\_M20; 1.  
 DR TIGRFAMs; TIGR01891; amidohydrolases; 1.  
 DR Carboxypeptidase; Complete proteome.  
 SQ SEQUENCE 404 AA; 44080 MW; 4DBBBE73321C7327 CRC64;

Query Match 49.0%; Score 48; DB 2; Length 404;  
 Best Local Similarity 61.8%; Pred. No. 94;  
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 IPDNAVLEGSIL 12  
 Db 261 IPDNMLLEGTLL 271

Search completed: March 11, 2006, 05:08:40

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RESULT 4  
AD056196  
ID AD056196 standard; protein, 343 AA.  
XX  
AC AD056196;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Sporobolomyces salmonicolor ketoreductase, aldehyde reductase II.  
XX  
KM (R)-hydroxy ester; alpha-keto ester; ketoreductase; enzyme;  
XX aldehyde reductase II.  
XX Sporidiobolus salmonicolor.  
XX OS Sporidiobolus salmonicolor.  
XX PN US2004101937-A1.  
XX PD 27-MAY-2004.  
XX PP 08-JUL-2003; 2003US-00616320.  
XX PR 10-JUL-2002; 2002US-0394761P.  
XX PA (MOOR/) MOORE J C.  
XX PA (STUR/) STURR M G.  
XX PA (MCLA/) MCLAUGHLIN K.  
XX PA (KIMJ/) KIM J.  
XX PI Moore JC, Sturr MG, McLaughlin K, Kim J;  
XX DR WPI; 2004-431257/40.  
XX PT Preparing (R)-hydroxy ester involves adding alpha-keto ester to mixture  
XX comprising ketoreductase enzyme and non-ketoreductase enzyme components.  
XX PS Discloure; SEQ ID NO 3; 10pp; English.  
XX CC The invention relates to a method of preparing high yields of an (R)-  
XX hydroxy ester by reducing an alpha-keto ester using a ketoreductase  
XX enzyme. The present sequence represents Sporobolomyces salmonicolor  
XX ketoreductase, aldehyde reductase II used in the method of the invention.  
XX CC Sequence 343 AA;  
SQ  
Query Match 100.0%; Score 107; DB 8; Length 343;  
Best Local Similarity 100.0%; Pred. No. 2.2e-08;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 MAKIDNAVLPEGSLVLTGANG 22  
DB 1 MAKIDNAVLPEGSLVLTGANG 22  
RESULT 5  
AD056197  
ID AD056197 standard; peptide; 21 AA.  
XX  
AC AD056197;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Sporobolomyces salmonicolor aldehyde reductase II, N-terminal peptide #3.  
XX  
KM (R)-hydroxy ester; alpha-keto ester; ketoreductase; enzyme;  
XX aldehyde reductase II.  
XX Sporidiobolus salmonicolor.  
XX OS Sporidiobolus salmonicolor.  
XX PN US2004101937-A1.  
XX PD 27-MAY-2004.  
XX

PF 08-JUL-2003; 2003US-00616320.  
XX  
XX 10-JUL-2002; 2002US-0394761P.  
XX  
XX (MOOR/) MOORE J C.  
XX PA (STUR/) STURR M G.  
XX PA (MCLA/) MCLAUGHLIN K.  
XX PA (KIMJ/) KIM J.  
XX  
XX PI Moore JC, Sturr MG, McLaughlin K, Kim J;  
XX DR WPI; 2004-431257/40.  
XX PT Preparing (R)-hydroxy ester involves adding alpha-keto ester to mixture  
XX comprising ketoreductase enzyme and non-ketoreductase enzyme components.  
XX PS Claim 1; SEQ ID NO 4; 10pp; English.  
XX CC The invention relates to a method of preparing high yields of an (R)-  
XX hydroxy ester by reducing an alpha-keto ester using a ketoreductase  
XX enzyme. The present sequence represents a Sporobolomyces salmonicolor  
XX ketoreductase, aldehyde reductase II, N-terminal peptide used in the  
XX method of the invention.  
XX CC Sequence 21 AA;  
SQ  
Query Match 64.0%; Score 68.5; DB 8; Length 21;  
Best Local Similarity 81.8%; Pred. No. 0.0011;  
Matches 18; Conservative 0; Mismatches 3; Indels 1; Gaps 1;  
OY 1 MAKIDNAVLPEGSLVLTGANG 22  
DB 1 MAIPDNAVL-EGSLVKTGTGANG 21  
RESULT 6  
AD056194  
ID AD056194 standard; peptide; 20 AA.  
XX  
AC AD056194;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Sporobolomyces salmonicolor aldehyde reductase II, N-terminal peptide #1.  
XX  
KM (R)-hydroxy ester; alpha-keto ester; ketoreductase; enzyme;  
XX aldehyde reductase II.  
XX OS Sporidiobolus salmonicolor.  
XX PN US2004101937-A1.  
XX PD 27-MAY-2004.  
XX PP 08-JUL-2003; 2003US-00616320.  
XX PR 10-JUL-2002; 2002US-0394761P.  
XX PA (MOOR/) MOORE J C.  
XX PA (STUR/) STURR M G.  
XX PA (MCLA/) MCLAUGHLIN K.  
XX PA (KIMJ/) KIM J.  
XX PI Moore JC, Sturr MG, McLaughlin K, Kim J;  
XX DR WPI; 2004-431257/40.  
XX PT Preparing (R)-hydroxy ester involves adding alpha-keto ester to mixture  
XX comprising ketoreductase enzyme and non-ketoreductase enzyme components.  
XX PS Claim 1; SEQ ID NO 1; 10pp; English.  
XX CC The invention relates to a method of preparing high yields of an (R)-

CC hydroxy ester by reducing an alpha-keto ester using a ketoreductase  
 CC enzyme. The present sequence represents a Sporobolomyces salmonicolor  
 CC ketoreductase, aldehyde reductase II, N-terminal peptide used in the  
 CC method of the invention.

XX Sequence 20 AA;

QY Query Match 61.2%; Score 65.5; DB 8; Length 20;  
 Db Best Local Similarity 88.9%; Pred. No. 0.0032;  
 Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 5 DNAVLPFGSLVLTGANG 22  
 |||||  
 4 DNAVL-EGSLVKTGTGANG 20

RESULT 7  
 ADS25047 ID ADS25047 standard; protein; 323 AA.

AC ADS25047;

DT 02-DEC-2004 (first entry)

DE Bacterial polypeptide #14080.

XX Recombinant DNA construct; transformed plant; improved plant property;  
 KM cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;  
 KM pathogen tolerance; pest tolerance; plant disease resistance;  
 KM cell cycle pathway modification; plant growth regulator;  
 KM homologous recombination; seed oil yield; protein yield; carbohydrate;  
 KM nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
 KM bacterial polypeptide.

XX Bacteria.

PN US2003233675-A1.

XX 18-DEC-2003.

PF 20-FEB-2003; 2003US-00369493.

PR 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.

PA (HINKLE/) HINKLE G J.

PA (SLATER/) SLATER S C.

PA (CHEN/) CHEN X.

PA (GOLD/) GOLDMAN B S.

PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide  
 PT for expression of a polynucleotide encoding a polypeptide from a  
 PT microbial source, useful for producing plants with improved properties.

XX Claim 1; SEQ ID NO 14080, 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a  
 CC promoter functional in a plant cell, where the promoter is positioned to  
 CC provide for expression of a polynucleotide encoding a polypeptide from a  
 CC microbial source. The invention also relates to a transformed plant  
 CC comprising the recombinant DNA construct and a method of producing a  
 CC transformed plant having an improved property. The plant is a crop plant  
 CC such as maize or soybean. The method of producing a transformed plant  
 CC having an improved property comprises transforming a plant with the  
 CC recombinant DNA construct and growing the transforming plant, where the  
 CC polynucleotide or polypeptide is useful for improving plant properties.  
 CC The recombinant DNA construct is useful for producing plants with  
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,

CC increased resistance to plant disease, better growth rate by modification  
 CC of the cell cycle pathway with plant growth regulators, increased rate of  
 CC homologous recombination, modified seed oil or protein yield and/or  
 CC content, improved yield by modification of carbohydrate, nitrogen or  
 CC phosphorus use and/or uptake, by modification of photosynthesis or by  
 CC providing improved plant growth and development under at least one stress  
 CC condition, improved lignin production or improved galactomannan  
 CC production. This sequence represents a bacterial polypeptide used in the  
 CC scope of the invention. Note: The sequence data for this patent did not  
 CC form part of the printed specification but was obtained in electronic  
 CC format from USPTO at [seqdata.uspto.gov/Sequence.html](http://seqdata.uspto.gov/Sequence.html).

XX Sequence 323 AA;

QY Query Match 50.5%; Score 54; DB 8; Length 323;  
 Db Best Local Similarity 59.1%; Pred. No. 6.2; 8; Indels 0; Gaps 0;  
 Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAKIDNAVLPFGSLVLTGANG 22  
 |||||  
 137 MALEBNGVTPQGEVLVTGANG 158

RESULT 8  
 AAY38793 ID AAY38793 standard; protein; 461 AA.

AC AAY38793;

DT 08-OCT-1999 (first entry)

DE Neisseria gonorrhoeae antigenic protein encoded by ORF140.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
 KM treatment; Neisseria infection; meningitis; septicemia; gonorrhea.

OS Neisseria gonorrhoeae.

PN WO9924578-A2.

XX 20-MAY-1999.

PF 09-OCT-1998; 98WO-1B001665.

PR 06-NOV-1997; 97GB-00023516.

PR 14-NOV-1997; 97GB-00024190.

PR 18-NOV-1997; 97GB-00024386.

PR 27-NOV-1997; 97GB-00025158.

PR 10-DEC-1997; 97GB-00026147.

PR 14-JAN-1998; 98GB-00000759.

PR 01-SEP-1998; 98GB-00019016.

XX (CHIR-) CHIRON SPA.

PI Masignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;

XX WPI; 1999-327407/27.

PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for  
 PT diagnosis, treatment and prevention of infection.

XX Claim 4; Page 336; 524pp; English.

CC Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and  
 CC N. gonorrhoeae antigenic proteins. They are encoded by open reading  
 CC frames (ORFs) AAZ11972-Z12358. The antigenic proteins, their fragments,  
 CC their nucleic acids and antibodies are used for diagnosis, prevention (as  
 CC vaccines) or treatment of Neisseria infections, such as meningitis,  
 CC septicemia and gonorrhea. Both organisms are closely related. Fragments  
 CC of the nucleic acids are useful as hybridisation probes and antisense  
 CC reagents  
 XX Sequence 461 AA;

[illegible]

ID	ABE49406 standard; protein; 461 AA.
XX	
AC	ABE49406;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	N. gonorrhoeae protein SEQ ID NO 592.
XX	
KW	antibacterial; immunosuppressive; antiinflammatory; vaccine;
KM	neisseria gonorrhoeae infection; gynecological; infection;
KW	neisseria meningitidis infection; meningitis; neuroprotective;
KM	inflammation; neurological disease; sepsis; diagnosis.
XX	
OS	Neisseria gonorrhoeae.
XX	
FN	US6914131-B1.
XX	
PD	05-JUL-2005.
XX	
PE	30-APR-1999; 99US-00303518.
XX	
PR	09-OCT-1998; 98WO-IB001665.
XX	
PA	(CHIR ) CHIRON SRL.
XX	
PI	Scarlatto V, Maignani V, Rappuoli R, Pizzo M, Grandi G;
XX	
DR	WPI; 2005-464877/47.
XX	
DR	N-PSDB; ABE49405.
XX	
PT	New Neisserial nucleic acids useful for diagnosing and/or treating
PT	bacterial infections, in particular meningitis and septicemia caused by
PT	Neisseria meningitidis and Neisseria gonorrhea.
XX	
PS	Example 70; SEQ ID NO 592; 613bp; English.
XX	
CC	The invention relates to an isolated nucleic acid molecule. The methods
CC	and compositions of the present invention are useful for diagnosing
CC	and/or treating Neisserial bacterial infections, in particular meningitis
CC	and septicemia caused by Neisseria meningitidis and Neisseria gonorrhea.
CC	The present sequence represents the amino acid sequence of a N.
CC	gonorrhoeae protein. Note: The sequence data for this patent did not form
CC	part of the printed specification, but was obtained in electronic format
CC	directly from USPTO at seqdata.uspto.gov/sequence.html?docID=6914131B1.
XX	
SQ	Sequence 461 AA;
XX	
Query Match	48.6%; Score 52; DB 9; Length 461;
Best Local Similarity	47.4%; Pred.No. 20;
Matches	9; Conservative 5; Mismatches 5; Indels 0; Gaps 0
OY	4 IDNAVLPGSLVLTGTANG 22     :   :   :   :   Db 312 VDGAALPACSVILRTGAGG 330
RESULT 11	
AEBA9404	
ID	AEBA9404 strand; protein; 461 AA.
XX	
AC	AEBA9404;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	N. gonorrhoeae protein SEQ ID NO 590.
XX	
KW	antibacterial; immunosuppressive; antiinflammatory; vaccine;
KM	neisseria gonorrhoeae infection; gynecological; infection;
KW	neisseria meningitidis infection; meningitis; neuroprotective;
KM	inflammation; neurological disease; sepsis; diagnosis.
XX	
OS	Neisseria gonorrhoeae.
XX	

PN US6914131-B1.  
XX  
PD 05-JUL-2005.  
XX  
PF 30-APR-1999; 99US-00303518.  
XX  
PR 09-OCT-1998; 98WO-IB001665.  
XX  
PA (CHIR ) CHIRON SRL.  
PI Scarlato V, Maignani V, Rappuoli R, Pizza M, Grandi G,  
XX  
DR WPI; 2005-464877/47.  
XX  
PT New Neisserial nucleic acids useful for diagnosing and/or treating  
PT bacterial infections, in particular meningitis and septicemia caused by  
XX Neisseria meningitidis and Neisseria gonorrhoea.  
XX  
PS Example 70; SEQ ID NO 590; 613pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule. The methods  
CC and compositions of the present invention are useful for diagnosing  
CC and/or treating Neisserial bacterial infections, in particular meningitis  
CC and septicemia caused by Neisseria meningitidis and Neisseria gonorrhoea.  
CC The present sequence represents the amino acid sequence of a N.  
CC gonorrhoeae protein. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from USPTO at [seqdata.uspto.gov/sequence.html?docID=6914131B1](http://seqdata.uspto.gov/sequence.html?docID=6914131B1).  
XX  
SQ Sequence 461 AA;  
XX  
Query Match 48.6%; Score 52; DB 9; Length 461;  
Best Local Similarity 47.4%; Pred. No. 20;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
XX  
CY 4 IDNAVLPEGSLVLTGANG 22  
Db 312 VDGLALPACSVILITGAGG 330  
XX  
RESULT 12  
ABP77208  
ID ABP77208 standard; protein; 485 AA.  
XX  
AC ABP77208;  
XX  
DT 07-MAR-2003 (first entry)  
XX  
DE N. gonorrhoeae amino acid sequence SEQ ID 946.  
XX  
KM Antibacterial; infection; vaccine; gene therapy.  
XX  
OS Neisseria gonorrhoeae.  
XX  
PN WO200279243-A2.  
XX  
PD 10-OCT-2002.  
XX  
PF 12-FEB-2002; 2002WO-IB002069.  
XX  
PR 12-FEB-2001; 2001GB-00003424.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
PI Fontana MR, Pizza M, Maignani V, Monaci E;  
XX  
DR WPI; 2003-058415/05.  
XX  
PR N-PSDB; ABZ38178.  
XX  
PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a  
PT medicament for treating or preventing N. gonorrhoeae infection.  
XX  
PS Disclosure; Page 257; 815pp; English.

XX  
CC The present invention relates to proteins from Neisseria gonorrhoeae.  
CC Also disclosed are the nucleic acid molecules encoding the proteins and  
CC antibodies that specifically bind to the proteins. The composition  
CC comprising the protein, nucleic acid or antibody is useful for the  
CC manufacture of a medicament for treating or preventing N. gonorrhoeae  
CC infection, this may be in the form of a vaccine or gene therapy.  
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid  
CC molecules of the invention  
XX  
SQ Sequence 485 AA;  
XX  
Query Match 48.6%; Score 52; DB 6; Length 485;  
Best Local Similarity 47.4%; Pred. No. 21;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
XX  
CY 4 IDNAVLPEGSLVLTGANG 22  
Db 336 VDGLALPACSVILITGAGG 354  
XX  
RESULT 13  
AAV38791  
ID AAV38791 standard; protein; 461 AA.  
XX  
AC AAV38791;  
XX  
DT 08-OCT-1999 (first entry)  
XX  
DE Neisseria meningitidis antigen encoded by ORF140.  
XX  
KM Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
KM treatment; Neisseria infection; meningitis; septicemia; gonorrhoea.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9924578-A2.  
XX  
PD 20-MAY-1999.  
XX  
PF 09-OCT-1998; 98WO-IB001665.  
XX  
PR 06-NOV-1997; 97GB-00023516.  
PR 14-NOV-1997; 97GB-00024190.  
PR 16-NOV-1997; 97GB-00024386.  
PR 27-NOV-1997; 97GB-00025158.  
PR 10-DEC-1997; 97GB-00026147.  
PR 14-JAN-1998; 98GB-00000759.  
PR 01-SEP-1998; 98GB-00019016.  
XX  
PA (CHIR-) CHIRON SPA.  
XX  
PI Maignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;  
XX  
DR WPI; 1999-327407/27.  
XX  
PR P-PSDB; AAV38791.  
XX  
PT Proteins from Neisseria meningitidis and N. gonorrhoeae useful for  
PT diagnosis, treatment and prevention of infection.  
XX  
PS Claim 4; Page 334; 524pp; English.  
XX  
CC Amino acid sequences AAV38499-Y38944 represent Neisseria meningitidis and  
CC N. gonorrhoeae antigenic proteins. They are encoded by open reading  
CC frames (ORFs) AA211972-Z12358. The antigenic proteins, their fragments, (as  
CC their nucleic acids and antibodies are used for diagnosis, prevention (as  
CC vaccines) or treatment of Neisseria infections, such as meningitis,  
CC septicemia and gonorrhoea. Both organisms are closely related. Fragments  
CC of the nucleic acids are useful as hybridisation probes and antisense  
CC reagents  
XX  
SQ Sequence 461 AA;

Query Match 47.7%; Score 51; DB 2; Length 461;  
Best Local Similarity 47.4%; Pred. No. 29;  
Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 IDNAVLPESGLVLTGANG 22  
DB 312 VDGLAPVCVILITGAGG 330

RESULT 14  
ID AAY38792 standard; protein; 461 AA.  
XX AAY38792;

XX 08-OCT-1999 (first entry)

XX Neisseria meningitidis strain A antigen encoded by ORF140.

XX Neisseria meningitidis; Neisseria gonorrhoeae; antigen; vaccine;  
XX treatment; Neisseria infection; meningitis; septicemia; gonorrhea.

XX Neisseria meningitidis.

XX WO9924578-A2.

XX 20-MAY-1999.

XX 09-OCT-1998; 98WO-IB001665.

XX 06-NOV-1997; 97GB-00023516.

XX 14-NOV-1997; 97GB-00024190.

XX 18-NOV-1997; 97GB-00024386.

XX 27-NOV-1997; 97GB-00025158.

XX 10-DEC-1997; 97GB-00026147.

XX 14-JAN-1998; 98GB-00000755.

XX 01-SEP-1998; 98GB-00019016.

XX (CHIR-) CHIRON SPA.

XX Maignani V, Rappuoli R, Pizza M, Scarlato V, Grandi G;

XX WPI, 1999-327407/27.

XX P-PSDB; AAY38792.

XX Proteins from Neisseria meningitidis and N. gonorrhoeae useful for

XX diagnosis, treatment and prevention of infection.

XX Claim 4; Page 335; 524pp; English.

XX Amino acid sequences AAY38499-Y38944 represent Neisseria meningitidis and

XX N. gonorrhoeae antigenic proteins. They are encoded by open reading

XX frames (ORFs) AA211972-212358. The antigenic proteins, their fragments,

XX their nucleic acids and antibodies are used for diagnosis, prevention (as

XX vaccines) or treatment of Neisseria infections, such as meningitis,

XX septicemia and gonorrhea. Both organisms are closely related. Fragments

XX of the nucleic acids are useful as hybridisation probes and antisense

XX reagents

XX Sequence 461 AA;

XX Query Match 47.7%; Score 51; DB 2; Length 461;

XX Best Local Similarity 47.4%; Pred. No. 29;

XX Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 IDNAVLPESGLVLTGANG 22

DB 312 VDGLAPVCVILITGAGG 330

RESULT 15

AEB49401 standard; protein; 461 AA.

XX AEB49401;

XX 22-SEP-2005 (first entry)

XX N. meningitidis protein SEQ ID NO 586.

XX antibacterial; immunosuppressive; antiinflammatory; vaccine;

XX Neisseria gonorrhoeae infection; gynecological; infection;

XX Neisseria meningitidis infection; meningitis; neuroprotective;

XX inflammation; neurological disease; sepsis; diagnosis.

XX Neisseria meningitidis.

XX US6914131-B1.

XX 05-JUL-2005.

XX 30-APR-1999; 99US-00303518.

XX 09-OCT-1998; 98WO-IB001665.

XX (CHIR ) CHIRON SRL.

XX Scarlato V, Maignani V, Rappuoli R, Pizza M, Grandi G;

XX WPI, 2005-464877/47.

XX N-PSDB; AEB49400.

XX New Neisserial nucleic acids useful for diagnosing and/or treating

XX bacterial infections, in particular meningitis and septicemia caused by

XX Neisseria meningitidis and Neisseria gonorrhea.

XX Example 70; SEQ ID NO 586; 613pp; English.

XX The invention relates to an isolated nucleic acid molecule. The methods

XX and compositions of the present invention are useful for diagnosing

XX and/or treating Neisserial bacterial infections, in particular meningitis

XX CC and septicemia caused by Neisseria meningitidis and Neisseria gonorrhea.

XX CC The present sequence represents the amino acid sequence of a N.

XX CC meningitidis protein. Note: The sequence data for this patent did not

XX CC form part of the printed specification, but was obtained in electronic

XX CC format directly from USPTO at

XX CC seqdata.uspto.gov/sequence.html?DocID=6914131B1.

XX Sequence 461 AA;

XX Query Match 47.7%; Score 51; DB 9; Length 461;

XX Best Local Similarity 47.4%; Pred. No. 29;

XX Matches 9; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 4 IDNAVLPESGLVLTGANG 22

DB 312 VDGLAPVCVILITGAGG 330

Search completed: March 11, 2006, 05:02:25

Job time : 129.413 secs

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APPLICANT: Krogger, Burkhard  
APPLICANT: Schroder, Hartwig  
APPLICANT: Zeider, Oskar  
APPLICANT: Habermeyer, Gregor  
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL  
FILE REFERENCE: BGI-129CP  
CURRENT APPLICATION NUMBER: US/09/605,703B  
CURRENT FILING DATE: 2000-06-27  
PRIOR APPLICATION NUMBER: 60/142,764  
PRIOR FILING DATE: 1999-07-08  
PRIOR APPLICATION NUMBER: 60/152,318  
PRIOR FILING DATE: 1999-09-03  
NUMBER OF SEQ ID NOS: 2934  
SEQ ID NO 2064  
LENGTH: 340  
TYPE: PRT  
ORGANISM: Corynebacterium glutamicum  
US-09-605-703B-2064

Query Match 45.8%; Score 49; DB 2; Length 340;  
Best Local Similarity 42.9%; Pred. No. 9.4;  
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 AKIDNAVLPEGSGLVLTGANG 22  
DB 151 ALVGGIKPEDEGLVLTGSTG 171

RESULT 8  
US-09-489-039A-13937  
Sequence 13937, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 13937  
LENGTH: 687  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-13937

Query Match 44.9%; Score 48; DB 2; Length 687;  
Best Local Similarity 38.1%; Pred. No. 32;  
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

QY 2 AKIDNAVLPEGSGLVLTGANG 22  
DB 202 AIVDSGLVPEGLSLICGAG 222

RESULT 9  
US-09-543-681A-6546  
Sequence 6546, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543,681A  
CURRENT FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128,706  
PRIOR FILING DATE: 1999-04-09  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 6546

LENGTH: 449  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-6546

Query Match 43.9%; Score 47; DB 2; Length 449;  
Best Local Similarity 56.2%; Pred. No. 28;  
Matches 9; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 AVLPEGSGLVLTGANG 22  
DB 303 AIDPAGITLLVLTGANG 318

RESULT 10  
US-09-252-991A-27987  
Sequence 27987, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 31142  
SEQ ID NO 27987  
LENGTH: 675  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-27987

Query Match 43.9%; Score 47; DB 2; Length 675;  
Best Local Similarity 61.1%; Pred. No. 46;  
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 DNAMLPEGSGLVLTGANG 22  
DB 226 DAVIDPEGRLEGGGLDG 243

RESULT 11  
US-09-078-347A-1  
Sequence 1, Application US/09078347A  
Patent No. 6132968  
GENERAL INFORMATION:  
APPLICANT: Le, Xiao-Chun  
APPLICANT: Weinfield, Michael  
APPLICANT: Xing, James Z.  
TITLE OF INVENTION: Methods for Quantitating Low Level  
TITLE OF INVENTION: Modifications of Nucleotide Sequences  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Medlen & Carroll, LLP  
STREET: 220 Montgomery Street, Suite 2200  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/078,347A  
FILING DATE: 13-MAY-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Carroll, Peter G.  
REGISTRATION NUMBER: 32,837  
REFERENCE/DOCKET NUMBER: UALB-03283  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 705-8410  
TELEFAX: (415) 397-8338  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 940 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-09-078-347A-1

Query Match 43.0%; Score 46; DB 2; Length 940;  
Best Local Similarity 47.1%; Pred. No. 1e+02;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 NAVLPESGLVLTGANG 22  
DB 18 NLVIPRDKLIVTGLSG 34

RESULT 12  
US-09-651-656-101  
Sequence 101, Application US/09651656  
Patent No. 6340566  
GENERAL INFORMATION:  
APPLICANT: MCCUTHEN-MALONEY, SANDRA  
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY  
TITLE OF INVENTION: DETECTION AND QUANTITATION OF SINGLE NUCLEOTIDE  
TITLE OF INVENTION: POLYMORPHISMS, DNA SEQUENCE VARIATIONS, DNA MUTATIONS,  
FILE REFERENCE: IL-10689  
CURRENT APPLICATION NUMBER: US/09/651,656  
CURRENT FILING DATE: 2000-08-29  
PRIOR APPLICATION NUMBER: 60/192,764  
PRIOR FILING DATE: 2000-03-28  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 101  
LENGTH: 940  
TYPE: PRN  
ORGANISM: Escherichia coli  
US-09-651-656-101

Query Match 43.0%; Score 46; DB 2; Length 940;  
Best Local Similarity 47.1%; Pred. No. 1e+02;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 NAVLPESGLVLTGANG 22  
DB 18 NLVIPRDKLIVTGLSG 34

RESULT 13  
US-09-650-855-101  
Sequence 101, Application US/09650855  
Patent No. 6365355  
GENERAL INFORMATION:  
APPLICANT: MCCUTHEN-MALONEY, SANDRA  
APPLICANT: LAWRENCE LIVERMORE NATIONAL LABORATORY  
TITLE OF INVENTION: CHIMERIC PROTEINS FOR DETECTION AND QUANTITATION OF DNA  
TITLE OF INVENTION: MUTATIONS, DNA SEQUENCE VARIATIONS, DNA DAMAGE AND DNA  
FILE REFERENCE: IL-10284  
CURRENT APPLICATION NUMBER: US/09/650,855  
CURRENT FILING DATE: 2000-08-29  
PRIOR APPLICATION NUMBER: 60/192,764  
PRIOR FILING DATE: 2000-03-28  
NUMBER OF SEQ ID NOS: 106  
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 101  
LENGTH: 940  
TYPE: PRN  
ORGANISM: Escherichia coli  
US-09-650-855-101

Query Match 43.0%; Score 46; DB 2; Length 940;  
Best Local Similarity 47.1%; Pred. No. 1e+02;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 NAVLPESGLVLTGANG 22  
DB 18 NLVIPRDKLIVTGLSG 34

RESULT 14  
US-09-489-039A-8607  
Sequence 8607, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 8607  
LENGTH: 941  
TYPE: PRN  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-8607

Query Match 43.0%; Score 46; DB 2; Length 941;  
Best Local Similarity 47.1%; Pred. No. 1e+02;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 NAVLPESGLVLTGANG 22  
DB 18 NLVIPRDKLIVTGLSG 34

RESULT 15  
US-09-134-000C-3792  
Sequence 3792, Application US/09134000C  
Patent No. 6617156  
GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
FILE REFERENCE: 032796-032  
CURRENT APPLICATION NUMBER: US/09/134,000C  
CURRENT FILING DATE: 1998-08-13  
PRIOR APPLICATION NUMBER: US 60/055,778  
PRIOR FILING DATE: 1997-08-15  
NUMBER OF SEQ ID NOS: 6812  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 3792  
LENGTH: 111  
TYPE: PRN  
ORGANISM: Enterococcus faecalis  
US-09-134-000C-3792

Query Match 42.1%; Score 45; DB 2; Length 111;  
Best Local Similarity 56.2%; Pred. No. 10;  
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 IDNAVLPESGLVLTG 19  
DB 55 VDPSPVPLGSLVTVSG 70



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Page 5

Search completed: March 11, 2006, 05:11:14  
Job time : 31.0317 secs

100-443887-100

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RESULT 7
US-10-616-320A-4
; Sequence 4, Application US/10616320A
; Publication No. US20040101937A1
; GENERAL INFORMATION:
; APPLICANT: Jeffrey C. Moore
; APPLICANT: Michael G. Sturt
; APPLICANT: Kathleen McLaughlin
; APPLICANT: Jaehon Kim
; TITLE OF INVENTION: PROCESS FOR REDUCING AN ALPHA-KETO ESTER
; FILE REFERENCE: 21115
; CURRENT APPLICATION NUMBER: US/10/616,320A
; CURRENT FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PRIMER
US-10-616-320A-4

Query Match      64.0%; Score 68.5; DB 4; Length 21;
Best Local Similarity 81.8%; Pred. No. 0.001;
Matches 18; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

QY      1 MAKIDNAVLPGSGSLVLTGTGANG 22
DB      1 MAIPDNNAVL-EGSLVKTGTGANG 21

RESULT 8
US-10-616-320A-1
; Sequence 1, Application US/10616320A
; Publication No. US20040101937A1
; GENERAL INFORMATION:
; APPLICANT: Jeffrey C. Moore
; APPLICANT: Michael G. Sturt
; APPLICANT: Kathleen McLaughlin
; APPLICANT: Jaehon Kim
; TITLE OF INVENTION: PROCESS FOR REDUCING AN ALPHA-KETO ESTER
; FILE REFERENCE: 21115
; CURRENT APPLICATION NUMBER: US/10/616,320A
; CURRENT FILING DATE: 2003-07-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PRIMER
US-10-616-320A-1

Query Match      61.2%; Score 65.5; DB 4; Length 20;
Best Local Similarity 88.9%; Pred. No. 0.0029;
Matches 16; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY      5 DNAVLPEGSLVLTGTGANG 22
DB      4 DNAVL-EGSLVKTGTGANG 20

RESULT 9
US-10-369-493-14080
; Sequence 14080, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.

APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14080
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-14080

Query Match      50.5%; Score 54; DB 4; Length 323;
Best Local Similarity 59.1%; Pred. No. 5.2;
Matches 13; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY      1 MAKIDNAVLPGSGSLVLTGTGANG 22
DB      137 MALERNGVTPQGGSLVLTGTGANG 158

RESULT 10
US-10-369-493-20309
; Sequence 20309, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 20309
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Pyrococcus horikoshii
US-10-369-493-20309

Query Match      45.8%; Score 49; DB 4; Length 339;
Best Local Similarity 64.7%; Pred. No. 35;
Matches 11; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      6 NAVALPEGSLVLTGTGANG 22
DB      164 NDALDEGSLVLTGTG 180

RESULT 11
US-09-738-626-6285
; Sequence 6285, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKOYO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
```

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FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 6285
LENGTH: 340
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6285

Query Match      45.8%; Score 49; DB 3; Length 340;
Best Local Similarity 42.9%; Pred. No. 35;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Cy      2 AKIDNAVLPEGSVLVTGANG 22
Db      151 ALVDQGIKPEDELTVTGSG 171

RESULT 12
US-10-282-122A-67877
Sequence 67877, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeeldeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/244,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remainder Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
SEQ ID NO 67877
LENGTH: 450
TYPE: PRT
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```
ORGANISM: Pseudomonas putida
US-10-282-122A-67877

Query Match      44.9%; Score 48; DB 4; Length 450;
Best Local Similarity 36.4%; Pred. No. 70;
Matches 8; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Cy      1 MAKIDNAVLPEGSVLVTGANG 22
Db      300 MKMLDQSLAPTAIVLVGAG 321

RESULT 13
US-10-662-358-1
Sequence 1, Application US/10662358
Publication No. US20050037473A1
GENERAL INFORMATION:
APPLICANT: Lee, Sang Yup
APPLICANT: PARK, Si Jae
TITLE OF INVENTION: PROCESS FOR PREPARING POLYHYDROXYALKANOATE EMPLOYING maoc GENE
FILE REFERENCE: 077446
CURRENT APPLICATION NUMBER: US/10/662,358
CURRENT FILING DATE: 2003-09-16
PRIOR APPLICATION NUMBER: KR 10-2003-0025863
PRIOR FILING DATE: 2003-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 681
TYPE: PRT
ORGANISM: Escherichia coli
US-10-662-358-1

Query Match      44.9%; Score 48; DB 5; Length 681;
Best Local Similarity 36.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

Cy      4 IDNAVLPEGSVLVTGANG 22
Db      198 VDSGLVPEGAISLIGCSAG 216

RESULT 14
US-10-450-763-39265
Sequence 39265, Application US/10450763
Publication No. US20050196754A1
GENERAL INFORMATION:
APPLICANT: Hyseng, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 39265
LENGTH: 1096
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (940)..(982)
OTHER INFORMATION: Aldehyde dehydrogenases glutamic acid proteins domain
OTHER INFORMATION: identified by EMATRIX, accession number BL00687B, p-value=1.675e-
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1096)
```





RESULT 7  
US-11-087-099-9804  
; Sequence 9804, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; PRIOR FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 9804  
; LENGTH: 174  
; TYPE: PRT  
; ORGANISM: Pseudomonas syringae pv. syringae B728a  
US-11-087-099-9804

Query Match 41.1%; Score 44; DB 7; Length 174;  
Best Local Similarity 57.1%; Pred. No. 7.5;  
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNAVPEGSVLVT 18  
:|:|:|:|:|:|  
DB 122 ENKVIPEGSLVMGT 135

RESULT 8  
US-11-082-389-168  
; Sequence 168, Application US/11082389  
; Publication No. US20050244935A1  
; GENERAL INFORMATION:  
; APPLICANT: Pompeius, Markus  
; APPLICANT: Krieger, Burkhard  
; APPLICANT: Schroeder, Hartwig  
; APPLICANT: Zeider, Oskar  
; APPLICANT: Haberhauser, Gregor  
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
; INVOLVED IN MEMBRANE SYNTHESIS AND MEMBRANE  
; TITLE OF INVENTION: TRANSPORT  
; FILE REFERENCE: BGI-131CPN  
; CURRENT APPLICATION NUMBER: US/11/082,389  
; PRIOR FILING DATE: 2005-03-16  
; PRIOR APPLICATION NUMBER: US 09/603024  
; PRIOR FILING DATE: 2000-06-23  
; PRIOR APPLICATION NUMBER: US 60/141031  
; PRIOR FILING DATE: 1999-06-25  
; PRIOR APPLICATION NUMBER: US 60/143262  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: US 60/151281  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: DE 19930487.4  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19930489.0  
; PRIOR FILING DATE: 1999-07-01  
; PRIOR APPLICATION NUMBER: DE 19931549.3  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19931550.7  
; PRIOR FILING DATE: 1999-07-08  
; PRIOR APPLICATION NUMBER: DE 19932134.5  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: DE 19941379.7  
; PRIOR FILING DATE: 1999-08-31  
; Remaining Prior Application data removed - See file wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 446  
; SEQ ID NO 168  
; LENGTH: 311  
; TYPE: PRT  
; ORGANISM: Corynebacterium glutamicum  
US-11-082-389-168

Query Match 41.1%; Score 44; DB 7; Length 311;

Best Local Similarity 50.0%; Pred. No. 15;  
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 9 LPEGSVLVTGANG 22  
:|:|:|:|:|:|  
DB 256 VPEGASTVITGPNG 269

RESULT 9  
US-10-873-528-162  
; Sequence 162, Application US/10873528  
; Publication No. US2005027681A1  
; GENERAL INFORMATION:  
; APPLICANT: Microbial Technics Limited  
; APPLICANT: Gilbert, Christophe FG  
; APPLICANT: Hansbro, Philip M  
; TITLE OF INVENTION: Proteins  
; FILE REFERENCE: PWC/P21129WO  
; CURRENT APPLICATION NUMBER: US/10/873,528  
; PRIOR FILING DATE: 2004-06-23  
; PRIOR APPLICATION NUMBER: US/09/769,787  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: GB 9816337.1  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: US 60/125164  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 388  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 162  
; LENGTH: 363  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-10-873-528-162

Query Match 41.1%; Score 44; DB 6; Length 363;  
Best Local Similarity 47.1%; Pred. No. 19;  
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 NAVLPEGSVLVTGANG 22  
:|:|:|:|:|:|  
DB 23 NITIPKGSFLTILGNSG 39

RESULT 10  
US-11-087-099-766  
; Sequence 766, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; PRIOR FILING DATE: 2005-03-22  
; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 766  
; LENGTH: 455  
; TYPE: PRT  
; ORGANISM: Clostridium acetobutylicum  
US-11-087-099-766

Query Match 41.1%; Score 44; DB 7; Length 455;  
Best Local Similarity 50.0%; Pred. No. 25;  
Matches 9; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 MAKIDNAVLPESGLVLT 18  
:|:|:|:|:|:|  
DB 348 IAVILNVIPEGSVFLIT 365

RESULT 11  
US-10-793-626-284  
; Sequence 284, Application US/10793626  
; Publication No. US2005025478A1

```
; GENERAL INFORMATION:
; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUB480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 284
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-10-793-626-284

Query Match          40.2%; Score 43; DB 6; Length 173;
Best Local Similarity 31.8%; Pred. No. 11;
Matches 7; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MAKIDNAVLPEGSILVLTGANG 22
Db 24 MKSVTHAIYPIGMWLLIIGGG 45

RESULT 12
US-11-096-568A-4407
; Sequence 4407, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4407
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(211)
; OTHER INFORMATION: Ceres Seq. ID no. 13637459
US-11-096-568A-4407

Query Match          40.2%; Score 43; DB 7; Length 211;
Best Local Similarity 47.1%; Pred. No. 14;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 NAVLPEGSILVLTGANG 22
Db 12 NVSLHDGALVLTGANG 28

RESULT 13
US-11-096-568A-4406
; Sequence 4406, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 4406
; LENGTH: 228
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; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(228)
; OTHER INFORMATION: Ceres Seq. ID no. 13637458
US-11-096-568A-4406

Query Match          40.2%; Score 43; DB 7; Length 228;
Best Local Similarity 47.1%; Pred. No. 15;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 6 NAVLPEGSILVLTGANG 22
Db 29 NVSLHDGALVLTGANG 45

RESULT 14
US-10-467-657-3300
; Sequence 3300, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04
; SEQ ID NO 3300
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3300

Query Match          40.2%; Score 43; DB 6; Length 241;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 DNAVLPEGSILVLTG 19
Db 58 DNALEKSGSLVMVG 72

RESULT 15
US-11-087-099-12277
; Sequence 12277, Application US/11087099
; Publication No. US20060041961A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53450)B EP
; CURRENT APPLICATION NUMBER: US/11/087,099
; CURRENT FILING DATE: 2005-03-22
; NUMBER OF SEQ ID NOS: 12464
; SEQ ID NO 12277
; LENGTH: 336
; TYPE: PRT
; ORGANISM: Thermoplasma acidophilum
US-11-087-099-12277

Query Match          40.2%; Score 43; DB 7; Length 336;
Best Local Similarity 56.2%; Pred. No. 24;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 AVLPEGSILVLTGANG 22
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Mon Mar 13 09:31:40 2006

us-10-616-320a-2.rapbn

Page 5

Db 159 AKVEGORVLITGAG 174

Search completed: March 11, 2006, 05:16:52  
Job time : 11.873 secs

119 1006 80000000

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